GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:56 ; Search time 363.973 Seconds
(without alignments)
836.639 Million cell updates/sec

Title: US-09-017-715A-2_COPY_120_127
Perfect score: 41
Sequence: 1 EEAQSGGD 8

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100744_25619/app_query.fasta_1.661
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_@CGN_1_1_5334_@runat_04052005_100744_25619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	41	100.0	233	2	BE171313	BE171313 RC1-HT054
c	2	41	100.0	301	1	AA055968	AA055968 zf22a02.s
	3	41	100.0	327	1	AA056035	AA056035 zf22a02.r
	4	41	100.0	333	4	BM748818	BM748818 K-EST0023
c	5	41	100.0	352	1	AI468480	AI468480 tg57g12.x
c	6	41	100.0	368	5	BU729743	BU729743 UI-E-CK1-
c	7	41	100.0	378	1	AA293803	AA293803 zt56h04.s
c	8	41	100.0	387	1	AA722407	AA722407 zg83h10.s
	9	41	100.0	393	1	AA394097	AA394097 zt56h04.r
c	10	41	100.0	404	7	CF529590	CF529590 UI-1-BC1p
	11	41	100.0	407	1	AV683707	AV683707 AV683707
c	12	41	100.0	408	1	AA946606	AA946606 oq38c12.s
c	13	41	100.0	412	1	AI139933	AI139933 qa68b04.x
	14	41	100.0	421	1	AV703171	AV703171 AV703171
	15	41	100.0	428	5	BX090816	BX090816 BX090816
c	16	41	100.0	438	1	AI684600	AI684600 wa84d12.x
c	17	41	100.0	438	1	AI936527	AI936527 wd29a07.x
c	18	41	100.0	442	1	AA804675	AA804675 of44b01.s
	19	41	100.0	451	4	BG826435	BG826435 602750062
	20	41	100.0	472	4	BM704200	BM704200 UI-E-CK1-
c	21	41	100.0	473	6	CA421283	CA421283 UI-H-FG0-
	22	41	100.0	474	4	BM706956	BM706956 UI-E-CQ0-
c	23	41	100.0	480	4	BM668990	BM668990 UI-E-CK1-
c	24	41	100.0	504	5	BU728272	BU728272 UI-E-CQ0-
	25	41	100.0	509	2	BE299889	BE299889 600944691
	26	41	100.0	510	2	BE298825	BE298825 601119383
c	27	41	100.0	519	1	AI016464	AI016464 ot78h06.s
	28	41	100.0	538	4	BM695726	BM695726 UI-E-CQ1-
c	29	41	100.0	544	4	BM665098	BM665098 UI-E-CQ1-
c	30	41	100.0	553	1	AA872836	AA872836 oh76f10.s
	31	41	100.0	555	5	BX474500	BX474500 DKFZp686D
	32	41	100.0	555	7	CV028548	CV028548 7090 Full
	33	41	100.0	558	4	BI548891	BI548891 603189023
	34	41	100.0	568	4	BG708703	BG708703 602674249
	35	41	100.0	578	5	BP212912	BP212912 BP212912
	36	41	100.0	582	5	BP197662	BP197662 BP197662
	37	41	100.0	583	5	BP200612	BP200612 BP200612
	38	41	100.0	583	5	BP346497	BP346497 BP346497
	39	41	100.0	584	1	AV708933	AV708933 AV708933
	40	41	100.0	584	5	BP201686	BP201686 BP201686
	41	41	100.0	588	4	BI755243	BI755243 603023269
c	42	41	100.0	592	6	CA443299	CA443299 UI-H-DH1-
c	43	41	100.0	593	6	CA443166	CA443166 UI-H-DH1-
c	44	41	100.0	614	5	BU730570	BU730570 UI-E-CI1-
c	45	41	100.0	617	1	AA633976	AA633976 ac33e03.s

ALIGNMENTS

RESULT 1
BE171313
LOCUS BE171313 233 bp mRNA linear EST 21-JUN-2000
DEFINITION RC1-HT0545-100300-012-g05 HT0545 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE171313
VERSION BE171313.1 GI:8634039
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 233)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-HT0545-100300-012-g05&t3=2000-03-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 4
High quality sequence stop: 233.

FEATURES Location/Qualifiers
source 1. .233
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0545"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	205	Length:	233
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x BE171313 (1-233)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db         93 GAGGAGGCCCAGAGTGGGGGAGAC 116
```

RESULT 2
AA055968/c
LOCUS AA055968 301 bp mRNA linear EST 17-SEP-1996
DEFINITION zf22a02.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377642 3', mRNA sequence.
ACCESSION AA055968
VERSION AA055968.1 GI:1548325
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 301)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham.

FEATURES Location/Qualifiers
source 1. .301
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1285898"
/db_xref="taxon:9606"
/clone="IMAGE:377642"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

ORIGIN

Alignment Scores:

Pred. No.:	266	Length:	301
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x AA055968 (1-301)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        301 GAGGAGGCCCAGAGTGGGGGAGAC 278
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RESULT 3
AA056035
LOCUS AA056035 327 bp mRNA linear EST 17-SEP-1996
DEFINITION zf22a02.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377642 5', mRNA sequence.
ACCESSION AA056035
VERSION AA056035.1 GI:1548374
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 296.

FEATURES Location/Qualifiers
source 1. .327
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1285898"
/db_xref="taxon:9606"
/clone="IMAGE:377642"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

ORIGIN

Alignment Scores:

Pred. No.:	290	Length:	327
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x AA056035 (1-327)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db         29 GAGGAGGCCCAGAGTGGGGGAGAC 52
```

RESULT 4
BM748818
LOCUS BM748818 333 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0023804 S9SNU601 Homo sapiens cDNA clone S9SNU601-1-C11 5', mRNA sequence.
ACCESSION BM748818
VERSION BM748818.1 GI:19078436
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 333)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: C column: 11
High quality sequence stop: 333.
FEATURES Location/Qualifiers
source 1. .333
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S9SNU601-1-C11"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="Top10F'"
/clone_lib="S9SNU601"
/note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.:	295	Length:	333
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x BM748818 (1-333)

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Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
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Db        237 GAGGAGGCCCAGAGTGGGGGAGAC 260
```

RESULT 5
AI468480/c
LOCUS AI468480 352 bp mRNA linear EST 30-MAR-1999
DEFINITION tg57g12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2112934 3' similar to TR:O15104 O15104 BCSG1 PROTEIN. ;, mRNA sequence.
ACCESSION AI468480
VERSION AI468480.1 GI:4330570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 352)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 430 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 323.
FEATURES Location/Qualifiers
source 1. .352
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2112934"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

```
Alignment Scores:
Pred. No.:              312          Length:        352
Score:                  41.00        Matches:       8
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            100.00%      Indels:        0
DB:                     1            Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x AI468480 (1-352)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        295 GAGGAGGCCCAGAGTGGGGGAGAC 272

RESULT 6
BU729743/c
LOCUS       BU729743                368 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  UI-E-CK1-afj-m-04-0-UI.s1 UI-E-CK1 Homo sapiens cDNA clone
            UI-E-CK1-afj-m-04-0-UI 3', mRNA sequence.
ACCESSION   BU729743
VERSION     BU729743.1  GI:23652933
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 368)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .368
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-CK1-afj-m-04-0-UI"
                     /tissue_type="Retina Foveal and Macular"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-CK1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-CK1 is a normalized cDNA library containing the
                     following tissue(s): Retina Foveal and Macular. The
                     library was constructed according to Bonaldo, Lennon and
                     Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is GTCC. This library was created for the program,
                     Gene Discovery in the Visual System, supported by National
                     Eye Institute (NEI).
                     TAG_TISSUE=Foveal and Macular Retina
                     TAG_LIB=UI-E-CK1
                     TAG_SEQ=GTCC"
ORIGIN

Alignment Scores:
Pred. No.:              327          Length:        368
Score:                  41.00        Matches:       8
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            100.00%      Indels:        0
DB:                     5            Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x BU729743 (1-368)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        320 GAGGAGGCCCAGAGTGGGGGAGAC 297

RESULT 7
AA293803/c
LOCUS       AA293803                378 bp    mRNA    linear   EST 12-AUG-1997
DEFINITION  zt56h04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:726391 3', mRNA sequence.
ACCESSION   AA293803
VERSION     AA293803.1  GI:1941726
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 378)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 484   Std Error: 0.00
            Seq primer: -41m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:5938504"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:726391"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
ORIGIN

Alignment Scores:
```

```
Pred. No.:              336          Length:        378
Score:                  41.00        Matches:       8
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            100.00%      Indels:        0
DB:                     1            Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x AA293803 (1-378)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        302 GAGGAGGCCCAGAGTGGGGGAGAC 279

RESULT 8
AA722407/c
LOCUS       AA722407                387 bp    mRNA    linear   EST 02-JAN-1998
DEFINITION  zg83h10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:400003 3', mRNA sequence.
ACCESSION   AA722407
VERSION     AA722407.1  GI:2740114
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 384.
FEATURES             Location/Qualifiers
     source          1. .387
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1307826"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:400003"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
ORIGIN

Alignment Scores:
Pred. No.:              344          Length:        387
Score:                  41.00        Matches:       8
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            100.00%      Indels:        0
DB:                     1            Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x AA722407 (1-387)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        297 GAGGAGGCCCAGAGTGGGGGAGAC 274

RESULT 9
AA394097
LOCUS       AA394097                393 bp    mRNA    linear   EST 12-AUG-1997
DEFINITION  zt56h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:726391 5' similar to TR:G971580 G971580 SENSORY NEURON
            SYNUCLEIN. ;, mRNA sequence.
ACCESSION   AA394097
VERSION     AA394097.1  GI:2047067
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 484   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .393
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:5938504"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:726391"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
ORIGIN

Alignment Scores:
Pred. No.:              349          Length:        393
Score:                  41.00        Matches:       8
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            100.00%      Indels:        0
DB:                     1            Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x AA394097 (1-393)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        111 GAGGAGGCCCAGAGTGGGGGAGAC 134
```

```
RESULT 10
CF529590/c
LOCUS       CF529590                404 bp    mRNA    linear   EST 11-SEP-2003
DEFINITION  UI-1-BC1p-asy-b-08-0-UI.s1 NCI_CGAP_Pl3 Homo sapiens cDNA clone
            UI-1-BC1p-asy-b-08-0-UI 3', mRNA sequence.
ACCESSION   CF529590
VERSION     CF529590.1  GI:34579285
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Brown
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .404
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-1-BC1p-asy-b-08-0-UI"
                     /tissue_type="Placenta"
                     /dev_stage="8-9 weeks"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Pl3"
                     /note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with
                     a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Pl3 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are GA, AGGAA. For
                     additional information, contact: Bento Soares,
                     bento-soares@uiowa.edu
                     TAG_TISSUE=placenta human 8 week
                     TAG_LIB=UI-1-BC1p
                     TAG_SEQ=GA"
ORIGIN

Alignment Scores:
Pred. No.:                359             Length:         404
Score:                    41.00           Matches:        8
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       7               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x CF529590 (1-404)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        321 GAGGAGGCCCAGAGTGGGGGAGAC 298

RESULT 11
AV683707
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LOCUS       AV683707                407 bp    mRNA    linear   EST 16-JAN-2002
DEFINITION  AV683707 GKC Homo sapiens cDNA clone GKCFPB06 5', mRNA sequence.
ACCESSION   AV683707
VERSION     AV683707.1  GI:10285570
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 407)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
  MEDLINE   21625106
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .407
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GKCFPB06"
                     /tissue_type="hepatocellular carcinoma"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GKC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                362             Length:         407
Score:                    41.00           Matches:        8
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       1               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AV683707 (1-407)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        169 GAGGAGGCCCAGAGTGGGGGAGAC 192

RESULT 12
AA946606/c
LOCUS       AA946606                408 bp    mRNA    linear   EST 23-JUL-1998
DEFINITION  oq38c12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1588630 3'
            similar to TR:O15104 O15104 BCSG1 PROTEIN. ;, mRNA sequence.
ACCESSION   AA946606
VERSION     AA946606.1  GI:3110001
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
```

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 812   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES              Location/Qualifiers
     source           1. .408
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1588630"
                      /tissue_type="2 pooled tumors (clear cell type)"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Kid5"
                      /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

Alignment Scores:
Pred. No.:                363            Length:         408
Score:                    41.00          Matches:        8
Percent Similarity:       100.00%        Conservative:   0
Best Local Similarity:    100.00%        Mismatches:     0
Query Match:              100.00%        Indels:         0
DB:                       1              Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AA946606 (1-408)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        309 GAGGAGGCCCAGAGTGGGGGAGAC 286

RESULT 13
AI139933/c
LOCUS       AI139933                412 bp    mRNA    linear   EST 05-OCT-1998
DEFINITION  qa68b04.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:1691887 3' similar to TR:O15104 O15104 BCSG1 PROTEIN. ;, mRNA
            sequence.
ACCESSION   AI139933
VERSION     AI139933.1  GI:3647390
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 584   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1691887"
                      /sex="unknown"
                      /dev_stage="19 weeks"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares_fetal_heart_NbHH19W"
                      /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library went through one round of
                      normalization to a Cot = 5. Library constructed by
                      M.Fatima Bonaldo. This library was constructed from the
                      same fetus as the fetal lung library, Soares fetal lung
                      NbHL19W."
ORIGIN

Alignment Scores:
Pred. No.:                367            Length:         412
Score:                    41.00          Matches:        8
Percent Similarity:       100.00%        Conservative:   0
Best Local Similarity:    100.00%        Mismatches:     0
Query Match:              100.00%        Indels:         0
DB:                       1              Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AI139933 (1-412)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        303 GAGGAGGCCCAGAGTGGGGGAGAC 280

RESULT 14
AV703171
LOCUS       AV703171                421 bp    mRNA    linear   EST 09-OCT-2000
DEFINITION  AV703171 ADB Homo sapiens cDNA clone ADBBCF03 5', mRNA sequence.
ACCESSION   AV703171
VERSION     AV703171.1  GI:10720500
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G.,
            Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z.,
            Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S.,
            Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
  TITLE     Homo sapiens cDNA ADB clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES              Location/Qualifiers
     source           1. .421
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="ADBBCF03"
                      /tissue_type="Adrenal gland"
                      /dev_stage="Adult"
                      /lab_host="SOLR"
                      /clone_lib="ADB"
                      /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
```

XhoI"
ORIGIN

Alignment Scores:
Pred. No.: 375 Length: 421
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-017-715A-2_COPY_120_127 (1-8) x AV703171 (1-421)

Qy 1 GluGluAlaGlnSerGlyGlyAsp 8
||||||||||||||||||||||||
Db 374 GAGGAGGCCCAGAGTGGGGGAGAC 397

RESULT 15
BX090816
LOCUS BX090816 428 bp mRNA linear EST 23-JAN-2003
DEFINITION BX090816 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGp998P081781 ; IMAGE:726391, mRNA sequence.
ACCESSION BX090816
VERSION BX090816.1 GI:27822248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 428)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998P081781.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
source 1. .428
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998P081781 ; IMAGE:726391"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
ORIGIN

Alignment Scores:
Pred. No.: 381 Length: 428
Score: 41.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-017-715A-2_COPY_120_127 (1-8) x BX090816 (1-428)

Qy 1 GluGluAlaGlnSerGlyGlyAsp 8
||||||||||||||||||||||||
Db 111 GAGGAGGCCCAGAGTGGGGGAGAC 134

Search completed: May 4, 2005, 13:46:36
Job time : 364.973 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:56 ; Search time 636.953 Seconds
(without alignments)
836.639 Million cell updates/sec

Title: US-09-017-715A-2_COPY_94_107
Perfect score: 70
Sequence: 1 VVRKEDLRPSAPQQ 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100744_25619/app_query.fasta_1.661
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_@CGN_1_1_5334_@runat_04052005_100744_25619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	70	100.0	161	2	BE774132	BE774132 MR1-UM000
	2	70	100.0	283	4	BM693306	BM693306 UI-E-CK1-
	3	70	100.0	333	4	BM748818	BM748818 K-EST0023
	4	70	100.0	369	1	AV708398	AV708398 AV708398
c	5	70	100.0	387	1	AA722407	AA722407 zg83h10.s
	6	70	100.0	393	1	AA394097	AA394097 zt56h04.r
	7	70	100.0	407	1	AV683707	AV683707 AV683707
c	8	70	100.0	412	1	AI139933	AI139933 qa68b04.x
	9	70	100.0	421	1	AV703171	AV703171 AV703171
	10	70	100.0	428	5	BX090816	BX090816 BX090816
c	11	70	100.0	438	1	AI684600	AI684600 wa84d12.x
c	12	70	100.0	442	1	AA804675	AA804675 of44b01.s
	13	70	100.0	451	4	BG826435	BG826435 602750062
	14	70	100.0	462	5	BX474511	BX474511 DKFZp686E
	15	70	100.0	467	6	CB107161	CB107161 K-EST0145
	16	70	100.0	472	4	BM704200	BM704200 UI-E-CK1-
	17	70	100.0	474	4	BM706956	BM706956 UI-E-CQ0-
c	18	70	100.0	480	4	BM668990	BM668990 UI-E-CK1-
	19	70	100.0	489	5	BP201709	BP201709 BP201709
c	20	70	100.0	504	5	BU728272	BU728272 UI-E-CQ0-
	21	70	100.0	509	2	BE299889	BE299889 600944691
	22	70	100.0	510	2	BE298825	BE298825 601119383
c	23	70	100.0	519	1	AI016464	AI016464 ot78h06.s
	24	70	100.0	538	4	BM695726	BM695726 UI-E-CQ1-
c	25	70	100.0	544	4	BM665098	BM665098 UI-E-CQ1-
	26	70	100.0	555	5	BX474500	BX474500 DKFZp686D
	27	70	100.0	555	7	CV028548	CV028548 7090 Full
	28	70	100.0	558	4	BI548891	BI548891 603189023
	29	70	100.0	568	4	BG708703	BG708703 602674249
	30	70	100.0	578	5	BP212912	BP212912 BP212912
	31	70	100.0	582	5	BP197662	BP197662 BP197662
	32	70	100.0	583	5	BP200612	BP200612 BP200612
	33	70	100.0	584	1	AV708933	AV708933 AV708933
	34	70	100.0	584	5	BP201686	BP201686 BP201686
	35	70	100.0	588	4	BI755243	BI755243 603023269
c	36	70	100.0	592	6	CA443299	CA443299 UI-H-DH1-
c	37	70	100.0	593	6	CA443166	CA443166 UI-H-DH1-
c	38	70	100.0	614	5	BU730570	BU730570 UI-E-CI1-
c	39	70	100.0	617	1	AA633976	AA633976 ac33e03.s
	40	70	100.0	617	4	BG707764	BG707764 602671103
	41	70	100.0	623	5	BP381244	BP381244 BP381244
	42	70	100.0	641	1	AL712443	AL712443 DKFZp686B
	43	70	100.0	653	4	BI757131	BI757131 603030894
	44	70	100.0	659	7	CN410061	CN410061 170006001
	45	70	100.0	706	4	BG328738	BG328738 602427017

ALIGNMENTS

RESULT 1
BE774132
LOCUS BE774132 161 bp mRNA linear EST 20-SEP-2000
DEFINITION MR1-UM0009-220500-015-g07_1 UM0009 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE774132
VERSION BE774132.1 GI:10227839
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 161)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR1-UM0009-220500-015-g07_1&t3=2000-05-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 161.

FEATURES Location/Qualifiers
source 1. .161
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UM0009"
/note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	0.0174	Length:	161
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x BE774132 (1-161)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db         69 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 110
```

RESULT 2
BM693306
LOCUS BM693306 283 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CK1-afm-i-14-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone UI-E-CK1-afm-i-14-0-UI 5', mRNA sequence.
ACCESSION BM693306
VERSION BM693306.1 GI:19006564
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers
source 1. .283
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CK1-afm-i-14-0-UI"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CK1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:

Pred. No.:	0.0316	Length:	283
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x BM693306 (1-283)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        229 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 270
```

RESULT 3
BM748818
LOCUS BM748818 333 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0023804 S9SNU601 Homo sapiens cDNA clone S9SNU601-1-C11 5', mRNA sequence.
ACCESSION BM748818
VERSION BM748818.1 GI:19078436
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 333)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: C column: 11
High quality sequence stop: 333.

FEATURES Location/Qualifiers
source 1. .333
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S9SNU601-1-C11"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"

/cell_line="SNU-601"
/lab_host="Top10F'"
/clone_lib="S9SNU601"
/note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
ORIGIN

Alignment Scores:

Pred. No.:	0.0375	Length:	333
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x BM748818 (1-333)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        159 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 200
```

RESULT 4
AV708398
LOCUS AV708398 369 bp mRNA linear EST 09-OCT-2000
DEFINITION AV708398 ADC Homo sapiens cDNA clone ADCAMB05 5', mRNA sequence.
ACCESSION AV708398
VERSION AV708398.1 GI:10725663
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
TITLE Homo sapiens cDNA ADC clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES Location/Qualifiers
source 1. .369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADCAMB05"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="ADC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:

Pred. No.:	0.0418	Length:	369
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x AV708398 (1-369)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369
```

RESULT 5
AA722407/c
LOCUS AA722407 387 bp mRNA linear EST 02-JAN-1998
DEFINITION zg83h10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:400003 3', mRNA sequence.
ACCESSION AA722407
VERSION AA722407.1 GI:2740114
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 387)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 384.
FEATURES Location/Qualifiers
source 1. .387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1307826"
/db_xref="taxon:9606"
/clone="IMAGE:400003"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
ORIGIN

Alignment Scores:

Pred. No.:	0.044	Length:	387
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0

```
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     1              Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AA722407 (1-387)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        375 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 334

RESULT 6
AA394097
LOCUS       AA394097                393 bp    mRNA    linear   EST 12-AUG-1997
DEFINITION  zt56h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:726391 5' similar to TR:G971580 G971580 SENSORY NEURON
            SYNUCLEIN. ;, mRNA sequence.
ACCESSION   AA394097
VERSION     AA394097.1  GI:2047067
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 484   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .393
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:5938504"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:726391"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
ORIGIN

Alignment Scores:
Pred. No.:              0.0447         Length:        393
Score:                  70.00          Matches:       14
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     1              Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AA394097 (1-393)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db         33 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 74

RESULT 7
AV683707
LOCUS       AV683707                407 bp    mRNA    linear   EST 16-JAN-2002
DEFINITION  AV683707 GKC Homo sapiens cDNA clone GKCFPB06 5', mRNA sequence.
ACCESSION   AV683707
VERSION     AV683707.1  GI:10285570
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 407)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
  MEDLINE   21625106
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .407
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GKCFPB06"
                     /tissue_type="hepatocellular carcinoma"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GKC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              0.0464         Length:        407
Score:                  70.00          Matches:       14
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     1              Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AV683707 (1-407)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 135

RESULT 8
AI139933/c
LOCUS       AI139933                412 bp    mRNA    linear   EST 05-OCT-1998
DEFINITION  qa68b04.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:1691887 3' similar to TR:O15104 O15104 BCSG1 PROTEIN. ;, mRNA
            sequence.
ACCESSION   AI139933
VERSION     AI139933.1  GI:3647390
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 584   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1691887"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
ORIGIN

Alignment Scores:
Pred. No.:                0.047          Length:          412
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x AI139933 (1-412)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        381 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 340

RESULT 9
AV703171
LOCUS       AV703171                421 bp    mRNA    linear   EST 09-OCT-2000
DEFINITION  AV703171 ADB Homo sapiens cDNA clone ADBBCF03 5', mRNA sequence.
ACCESSION   AV703171
VERSION     AV703171.1  GI:10720500
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G.,
            Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z.,
            Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S.,
            Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
  TITLE     Homo sapiens cDNA ADB clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ADBBCF03"
                     /tissue_type="Adrenal gland"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="ADB"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Alignment Scores:
Pred. No.:                0.0481         Length:          421
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x AV703171 (1-421)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        296 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 337

RESULT 10
BX090816
LOCUS       BX090816                428 bp    mRNA    linear   EST 23-JAN-2003
DEFINITION  BX090816 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGp998P081781 ; IMAGE:726391, mRNA sequence.
ACCESSION   BX090816
VERSION     BX090816.1  GI:27822248
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 428)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998P081781.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .428
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998P081781 ; IMAGE:726391"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
```

/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	0.0489	Length:	428
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x BX090816 (1-428)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db         33 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 74
```

RESULT 11
AI684600/c
LOCUS AI684600 438 bp mRNA linear EST 07-MAR-2000
DEFINITION wa84d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302871 3' similar to TR:O15104 O15104 BCSG1 PROTEIN. [1] ;, mRNA sequence.
ACCESSION AI684600
VERSION AI684600.1 GI:4895894
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 438)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 505 Std Error: 0.00
Seq primer: -40UP from Gibco.
FEATURES Location/Qualifiers
source 1. .438
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2302871"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	0.0502	Length:	438
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x AI684600 (1-438)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        378 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 337
```

RESULT 12
AA804675/c
LOCUS AA804675 442 bp mRNA linear EST 19-FEB-1998
DEFINITION of44b01.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1427017 3' similar to SW:SYUN_RAT Q63544 SENSORY NEURON SYNUCLEIN. ;, mRNA sequence.
ACCESSION AA804675
VERSION AA804675.1 GI:2876076
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Insert Length: 795 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 301.
FEATURES Location/Qualifiers
source 1. .442
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1427017"
/tissue_type="substantia nigra"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_CNS1"
/note="Organ: brain; Vector: pCMV-SPORT4; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.0 kb."

ORIGIN

Alignment Scores:

Pred. No.:	0.0506	Length:	442
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x AA804675 (1-442)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        391 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 350
```

RESULT 13
BG826435
LOCUS BG826435 451 bp mRNA linear EST 22-MAY-2001
DEFINITION 602750062F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4903046 5', mRNA sequence.
ACCESSION BG826435
VERSION BG826435.1 GI:14174022
KEYWORDS EST.

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1800  row: k  column: 15
            High quality sequence stop: 447.
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4903046"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_17"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Alignment Scores:
Pred. No.:                0.0517          Length:         451
Score:                    70.00           Matches:        14
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       4               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x BG826435 (1-451)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 390

RESULT 14
BX474511
LOCUS       BX474511                462 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686E24170_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686E24170 5', mRNA sequence.
ACCESSION   BX474511
VERSION     BX474511.1  GI:31668718
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 462)
  AUTHORS   Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686E24170) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .462
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686E24170"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

Alignment Scores:
Pred. No.:                0.0531          Length:         462
Score:                    70.00           Matches:        14
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       5               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x BX474511 (1-462)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        390 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 431

RESULT 15
CB107161
LOCUS       CB107161                467 bp    mRNA    linear   EST 28-JAN-2003
DEFINITION  K-EST0145400 L3SNU475 Homo sapiens cDNA clone L3SNU475-14-A11 5',
            mRNA sequence.
ACCESSION   CB107161
VERSION     CB107161.1  GI:27932968
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 14  row: A  column: 11
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1. .467
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L3SNU475-14-A11"
                     /sex="M"
                     /cell_line="SNU-475"
                     /lab_host="Top10F'"
                     /clone_lib="L3SNU475"
```

/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.:	0.0537	Length:	467
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x CB107161 (1-467)

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Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        412 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 453
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Search completed: May 4, 2005, 13:46:35
Job time : 639.953 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 10:17:21 ; Search time 113.879 Seconds
(without alignments)
748.404 Million cell updates/sec

Title: US-09-017-715A-2_COPY_94_107
Perfect score: 70
Sequence: 1 VVRKEDLRPSAPQQ 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100747_25719/app_query.fasta_1.661
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09017715_@CGN_1_1_684_@runat_04052005_100747_25719
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70	100.0	384	19	US-10-826-157-5	Sequence 5, Appli
2	70	100.0	479	10	US-09-918-995-2705	Sequence 2705, Ap
3	70	100.0	550	9	US-09-954-531-613	Sequence 613, App
4	70	100.0	550	17	US-10-453-478-1	Sequence 1, Appli
5	70	100.0	550	19	US-10-843-641A-1680	Sequence 1680, Ap
6	70	100.0	720	14	US-10-097-340-297	Sequence 297, App
7	70	100.0	720	17	US-10-282-174-469	Sequence 469, App
8	70	100.0	720	19	US-10-600-009-469	Sequence 469, App
9	70	100.0	796	9	US-09-925-298-171	Sequence 171, App
10	70	100.0	796	14	US-10-102-806-171	Sequence 171, App
11	53	75.7	478	9	US-09-925-298-172	Sequence 172, App
12	53	75.7	478	14	US-10-102-806-172	Sequence 172, App
13	53	75.7	4606	17	US-10-240-425-388	Sequence 388, App
14	53	75.7	5666	17	US-10-282-174-72	Sequence 72, Appl
15	53	75.7	5666	17	US-10-282-174-73	Sequence 73, Appl
16	53	75.7	5666	19	US-10-600-009-72	Sequence 72, Appl
17	53	75.7	5666	19	US-10-600-009-73	Sequence 73, Appl
18	53	75.7	6012	17	US-10-282-174-483	Sequence 483, App
19	53	75.7	6012	19	US-10-600-009-483	Sequence 483, App
c 20	48	68.6	135638	16	US-10-314-657-1	Sequence 1, Appli
c 21	48	68.6	135638	19	US-10-473-193-1	Sequence 1, Appli
c 22	47	67.1	657	17	US-10-282-122A-23679	Sequence 23679, A
c 23	46	65.7	794	18	US-10-425-115-165876	Sequence 165876,
24	45	64.3	435	18	US-10-425-115-141921	Sequence 141921,
c 25	45	64.3	465	9	US-09-864-761-6012	Sequence 6012, Ap
c 26	45	64.3	1077	13	US-10-027-632-101236	Sequence 101236,
c 27	45	64.3	1077	13	US-10-027-632-101237	Sequence 101237,
c 28	45	64.3	1077	17	US-10-027-632-101236	Sequence 101236,
c 29	45	64.3	1077	17	US-10-027-632-101237	Sequence 101237,
30	45	64.3	1410	17	US-10-282-122A-25555	Sequence 25555, A
31	45	64.3	1435	17	US-10-282-122A-26265	Sequence 26265, A
32	45	64.3	1473	17	US-10-282-122A-28635	Sequence 28635, A
33	45	64.3	1488	9	US-09-738-626-1425	Sequence 1425, Ap
34	45	64.3	1491	17	US-10-282-122A-17537	Sequence 17537, A
c 35	45	64.3	160103	17	US-10-085-117-262	Sequence 262, App
36	45	64.3	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 37	44	62.9	395	18	US-10-425-115-118311	Sequence 118311,
c 38	44	62.9	661	15	US-10-259-165-660	Sequence 660, App
39	44	62.9	775	17	US-10-424-599-9676	Sequence 9676, Ap
40	43	61.4	412	18	US-10-425-115-52591	Sequence 52591, A
41	43	61.4	465	9	US-09-864-761-4889	Sequence 4889, Ap
42	43	61.4	547	16	US-10-029-386-9553	Sequence 9553, Ap
c 43	43	61.4	571	9	US-09-864-761-9722	Sequence 9722, Ap
c 44	43	61.4	800	18	US-10-363-345A-37659	Sequence 37659, A
45	43	61.4	800	18	US-10-363-345A-37660	Sequence 37660, A

ALIGNMENTS

RESULT 1
US-10-826-157-5
; Sequence 5, Application US/10826157
; Publication No. US20050064548A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist, Susan L.
; APPLICANT: Outeiro, Tiago
; TITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
; TITLE OF INVENTION: PROCESSED PROTEINS AND USES THEREFOR
; FILE REFERENCE: 17481-003001
; CURRENT APPLICATION NUMBER: US/10/826,157
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/472,317
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 60/463,284
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 384

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-826-157-5

Alignment Scores:
Pred. No.:              0.00156        Length:         384
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     19             Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-826-157-5 (1-384)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
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Db        280 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 321

RESULT 2
US-09-918-995-2705
; Sequence 2705, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2705
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(479)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2705

Alignment Scores:
Pred. No.:              0.00193        Length:         479
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     10             Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-918-995-2705 (1-479)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        293 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 334

RESULT 3
US-09-954-531-613
; Sequence 613, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
;  APPLICANT: Weaver, Zoe
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Gene Sets
;  FILE REFERENCE: 689290-77
;  CURRENT APPLICATION NUMBER: US/09/954,531
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: US/60/233,133
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,009
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,034
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,509
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US/60/234,567
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 1392
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 613
;   LENGTH: 550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-531-613

Alignment Scores:
Pred. No.:              0.00222        Length:         550
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     9              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-954-531-613 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 4
US-10-453-478-1
; Sequence 1, Application US/10453478
; Publication No. US20030208043A1
;   GENERAL INFORMATION:
;        APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                   Jian Ni and Jing-Shan Hu
;        TITLE OF INVENTION: Human Genes, Sequences and
;                            Expression Products
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                        CECCHI, STEWART & OLSTEIN
;             STREET: 6 BECKER FARM ROAD
;             CITY: ROSELAND
;             STATE: NEW JERSEY
;             COUNTRY: USA
;             ZIP: 07068
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 INCH DISKETTE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: MS-DOS
;             SOFTWARE: WORD PERFECT 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/453,478
;             FILING DATE: 04-Jun-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/705,771
;             FILING DATE: August 30, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MULLINS, J.G.
;             REGISTRATION NUMBER: 33,073
;             REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 973-994-1700
;             TELEFAX: 973-994-1744
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 550 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-453-478-1
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Alignment Scores:
Pred. No.:                0.00222        Length:          550
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       17             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-453-478-1 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 5
US-10-843-641A-1680
; Sequence 1680, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;  APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US/09/954,531
;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1680
;   LENGTH: 550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-843-641A-1680

Alignment Scores:
Pred. No.:                0.00222        Length:          550
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       19             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-843-641A-1680 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
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Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 6
US-10-097-340-297
; Sequence 297, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
;  APPLICANT: John MONAHAN
;  APPLICANT:  Manjula GANNAVARAPU
;  APPLICANT:  Sebastian HOERSCH
;  APPLICANT:  Shubhangi KAMATKAR
;  APPLICANT:  Steve G. KOVATS
;  APPLICANT:  Rachel E. MEYERS
;  APPLICANT:  Michael MORRISEY
;  APPLICANT:  Peter OLANDT
;  APPLICANT:  Ami SEN
;  APPLICANT:  Peter VEIBY
;  APPLICANT:  Gordon B. MILLS
;  APPLICANT:  Robert C. BAST, Jr.
;  APPLICANT:  Karen LU
;  APPLICANT:  Rosemarie SCHMANDT
;  APPLICANT:  Xumei ZHAO
;  APPLICANT:  Karen GLATT
;  TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
;  TITLE OF INVENTION:  Assessment, Prevention, and Therapy of Ovarian Cancer
;  FILE REFERENCE: MRI-030
;  CURRENT APPLICATION NUMBER: US/10/097,340
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: 60/276,025
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/325,149
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/276,026
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/324,967
;  PRIOR FILING DATE: 2001/09/26
;  PRIOR APPLICATION NUMBER: 60/311,732
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/325,102
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/323,580
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 363
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-097-340-297

Alignment Scores:
Pred. No.:                0.00289        Length:          720
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       14             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-097-340-297 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 7
US-10-282-174-469
; Sequence 469, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
;  APPLICANT: Becker, Kenneth David
;  APPLICANT:  Velicelebi, Gonul
;  APPLICANT:  Elliot, Kathryn J.
;  APPLICANT:  Wang, Xin
;  APPLICANT:  Tanzi, Rudolph E.
;  APPLICANT:  Bertram, Lars
;  APPLICANT:  Saunders, Aleister J.
;  APPLICANT:  Mullin, Kristina M.
;  APPLICANT:  Sampson, Andrew Johnson
;  APPLICANT:  Blacker, Deborah Lynne
```

```
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
;  TITLE OF INVENTION:  ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
;  TITLE OF INVENTION:  NEURODEGENERATIVE DISEASES
;  FILE REFERENCE: 37481-3308
;  CURRENT APPLICATION NUMBER: US/10/282,174
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: US 60/339,525
;  PRIOR FILING DATE: 2001-10-25
;  PRIOR APPLICATION NUMBER: US 60/338,010
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/336,929
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/338,363
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/337,052
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/368,919
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 469
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 30,57,85,243,250,377,512,531,555,561,672
;   OTHER INFORMATION: N is any
US-10-282-174-469

Alignment Scores:
Pred. No.:              0.00289         Length:         720
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     17              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-282-174-469 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 8
US-10-600-009-469
; Sequence 469, Application US/10600009
; Publication No. US20050009031A1
; GENERAL INFORMATION:
;  APPLICANT: Becker, Kenneth David
;  APPLICANT:  Velicelebi, Gonul
;  APPLICANT:  Elliot, Kathryn J.
;  APPLICANT:  Wang, Xin
;  APPLICANT:  Tanzi, Rudolph E.
;  APPLICANT:  Bertram, Lars
;  APPLICANT:  Saunders, Aleister J.
;  APPLICANT:  Mullin, Kristina M.
;  APPLICANT:  Sampson, Andrew Johnson
;  APPLICANT:  Blacker, Deborah Lynne
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
;  TITLE OF INVENTION:  ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
;  TITLE OF INVENTION:  NEURODEGENERATIVE DISEASES
;  FILE REFERENCE: 37481-3308B
;  CURRENT APPLICATION NUMBER: US/10/600,009
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US 60/339,525
;  PRIOR FILING DATE: 2001-10-25
;  PRIOR APPLICATION NUMBER: US 60/338,010
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/336,929
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/338,363
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/337,052
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/368,919
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 10/282,174
;  PRIOR FILING DATE: 2002-10-25
;  NUMBER OF SEQ ID NOS: 564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 469
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 30,57,85,243,250,377,512,531,555,561,672
;   OTHER INFORMATION: N is any
US-10-600-009-469

Alignment Scores:
Pred. No.:              0.00289         Length:         720
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     19              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-600-009-469 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 9
US-09-925-298-171
; Sequence 171, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103
;  CURRENT APPLICATION NUMBER: US/09/925,298
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 796
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-298-171

Alignment Scores:
Pred. No.:              0.00319         Length:         796
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-925-298-171 (1-796)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        388 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 429

RESULT 10
US-10-102-806-171
; Sequence 171, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
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;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 796
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-102-806-171

Alignment Scores:
Pred. No.:              0.00319         Length:         796
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     14              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-102-806-171 (1-796)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        388 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 429

RESULT 11
US-09-925-298-172
; Sequence 172, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103
;  CURRENT APPLICATION NUMBER: US/09/925,298
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
;   LENGTH: 478
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-298-172

Alignment Scores:
Pred. No.:              2.27            Length:         478
Score:                  53.00           Matches:        10
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  90.91%          Mismatches:     0
Query Match:            75.71%          Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-925-298-172 (1-478)

Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||||
Db         80 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 112

RESULT 12
US-10-102-806-172
; Sequence 172, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
;   LENGTH: 478
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-102-806-172

Alignment Scores:
Pred. No.:              2.27            Length:         478
Score:                  53.00           Matches:        10
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  90.91%          Mismatches:     0
Query Match:            75.71%          Indels:         0
DB:                     14              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-102-806-172 (1-478)

Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||||
Db         80 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 112

RESULT 13
US-10-240-425-388
; Sequence 388, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Amanda
;  APPLICANT:  Boland, Joseph F.
;  APPLICANT:  Lord, Reginald V.
;  APPLICANT:  Alvarez, Chris
;  APPLICANT:  Wetzel, Jon C.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Vockley, Joseph G.
;  TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;  FILE REFERENCE: 44921-5026
;  CURRENT APPLICATION NUMBER: US/10/240,425
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: PCT/US01/09847
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/193,446
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 1588
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 388
;   LENGTH: 4606
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF044311
US-10-240-425-388

Alignment Scores:
Pred. No.:              21.1            Length:         4606
Score:                  53.00           Matches:        10
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  90.91%          Mismatches:     0
Query Match:            75.71%          Indels:         0
DB:                     17              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-240-425-388 (1-4606)
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Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||||
Db       3950 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 3982

RESULT 14
US-10-282-174-72
; Sequence 72, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
;  APPLICANT: Becker, Kenneth David
;  APPLICANT:  Velicelebi, Gonul
;  APPLICANT:  Elliot, Kathryn J.
;  APPLICANT:  Wang, Xin
;  APPLICANT:  Tanzi, Rudolph E.
;  APPLICANT:  Bertram, Lars
;  APPLICANT:  Saunders, Aleister J.
;  APPLICANT:  Mullin, Kristina M.
;  APPLICANT:  Sampson, Andrew Johnson
;  APPLICANT:  Blacker, Deborah Lynne
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
;  TITLE OF INVENTION:  ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
;  TITLE OF INVENTION:  NEURODEGENERATIVE DISEASES
;  FILE REFERENCE: 37481-3308
;  CURRENT APPLICATION NUMBER: US/10/282,174
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: US 60/339,525
;  PRIOR FILING DATE: 2001-10-25
;  PRIOR APPLICATION NUMBER: US 60/338,010
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/336,929
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/338,363
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/337,052
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/368,919
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 5666
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-282-174-72

Alignment Scores:
Pred. No.:                25.9          Length:          5666
Score:                    53.00         Matches:         10
Percent Similarity:       100.00%       Conservative:    1
Best Local Similarity:    90.91%        Mismatches:      0
Query Match:              75.71%        Indels:          0
DB:                       17            Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-282-174-72 (1-5666)

Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||||
Db       4512 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 4544

RESULT 15
US-10-282-174-73
; Sequence 73, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
;  APPLICANT: Becker, Kenneth David
;  APPLICANT:  Velicelebi, Gonul
;  APPLICANT:  Elliot, Kathryn J.
;  APPLICANT:  Wang, Xin
;  APPLICANT:  Tanzi, Rudolph E.
;  APPLICANT:  Bertram, Lars
;  APPLICANT:  Saunders, Aleister J.
;  APPLICANT:  Mullin, Kristina M.
;  APPLICANT:  Sampson, Andrew Johnson
;  APPLICANT:  Blacker, Deborah Lynne
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
;  TITLE OF INVENTION:  ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
;  TITLE OF INVENTION:  NEURODEGENERATIVE DISEASES
;  FILE REFERENCE: 37481-3308
;  CURRENT APPLICATION NUMBER: US/10/282,174
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: US 60/339,525
;  PRIOR FILING DATE: 2001-10-25
;  PRIOR APPLICATION NUMBER: US 60/338,010
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/336,929
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/338,363
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/337,052
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/368,919
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
;   LENGTH: 5666
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 560,590,617,645,915,987,1723,1943,1950,3151,3178,3189,3284,
;   LOCATION: 4276,4311,4552,4995,5019,5025,5112,5136,5421,5648,5517
;   OTHER INFORMATION: N is any
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 3779
;   OTHER INFORMATION: deletion: T
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 4156
;   OTHER INFORMATION: insertion following nucleotide 4155
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 4976
;   OTHER INFORMATION: deletion: C
US-10-282-174-73

Alignment Scores:
Pred. No.:                25.9          Length:          5666
Score:                    53.00         Matches:         10
Percent Similarity:       100.00%       Conservative:    1
Best Local Similarity:    90.91%        Mismatches:      0
Query Match:              75.71%        Indels:          0
DB:                       17            Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-10-282-174-73 (1-5666)

Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
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Db       4512 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 4544


Search completed: May  4, 2005, 16:39:43
Job time : 126.546 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:55 ; Search time 32.4161 Seconds
(without alignments)
706.682 Million cell updates/sec

Title: US-09-017-715A-2_COPY_94_107
Perfect score: 70
Sequence: 1 VVRKEDLRPSAPQQ 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100745_25632/app_query.fasta_1.661
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_@CGN_1_1_116_@runat_04052005_100745_25632 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	70	100.0	550	3	US-08-705-771-1	Sequence 1, Appli
	2	70	100.0	550	4	US-09-417-540-1	Sequence 1, Appli
	3	70	100.0	702	4	US-09-949-016-1915	Sequence 1915, Ap
	4	70	100.0	720	4	US-09-949-016-442	Sequence 442, App
	5	53	75.7	8607	4	US-09-949-016-13657	Sequence 13657, A
	6	53	75.7	8608	4	US-09-949-016-12184	Sequence 12184, A
c	7	47	67.1	825	4	US-09-489-039A-172	Sequence 172, App
c	8	45	64.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	9	45	64.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	10	43	61.4	1011	4	US-09-902-540-8804	Sequence 8804, Ap
	11	43	61.4	1187	1	US-08-440-856A-2	Sequence 2, Appli
c	12	43	61.4	10096	4	US-09-902-540-935	Sequence 935, App
	13	42	60.0	689	4	US-09-949-016-5443	Sequence 5443, Ap
	14	42	60.0	690	3	US-09-419-568F-24	Sequence 24, Appl
	15	42	60.0	690	3	US-09-354-243B-24	Sequence 24, Appl
	16	42	60.0	1152	4	US-09-870-574-1	Sequence 1, Appli
	17	42	60.0	4797	3	US-09-419-568F-25	Sequence 25, Appl
	18	42	60.0	4797	3	US-09-354-243B-25	Sequence 25, Appl
	19	42	60.0	8888	4	US-09-949-016-17185	Sequence 17185, A
c	20	42	60.0	50950	4	US-09-949-016-16659	Sequence 16659, A
c	21	41.5	59.3	9005	4	US-09-902-540-7894	Sequence 7894, Ap
c	22	41.5	59.3	10793	4	US-09-902-540-1062	Sequence 1062, Ap
c	23	41	58.6	601	4	US-09-949-016-115274	Sequence 115274,
c	24	41	58.6	601	4	US-09-949-016-144544	Sequence 144544,
c	25	41	58.6	918	4	US-09-902-540-9560	Sequence 9560, Ap
	26	41	58.6	1073	1	US-08-356-405-8	Sequence 8, Appli
	27	41	58.6	1074	4	US-09-826-509-446	Sequence 446, App
	28	41	58.6	1545	4	US-09-270-767-1178	Sequence 1178, Ap
	29	41	58.6	1545	4	US-09-270-767-16460	Sequence 16460, A
c	30	41	58.6	2128	3	US-09-280-116-11	Sequence 11, Appl
c	31	41	58.6	2217	1	US-07-865-662F-9	Sequence 9, Appli
c	32	41	58.6	2217	3	US-08-374-219B-9	Sequence 9, Appli
c	33	41	58.6	2459	3	US-09-443-795-2	Sequence 2, Appli
	34	41	58.6	7386	4	US-09-949-016-13287	Sequence 13287, A
	35	41	58.6	8268	1	US-08-375-709-10	Sequence 10, Appl
	36	41	58.6	8268	1	US-08-752-929-10	Sequence 10, Appl
	37	41	58.6	8268	4	US-09-231-899-83	Sequence 83, Appl
	38	41	58.6	15172	4	US-09-902-540-1086	Sequence 1086, Ap
c	39	41	58.6	15661	4	US-09-949-016-13161	Sequence 13161, A
c	40	41	58.6	18200	4	US-09-949-016-15660	Sequence 15660, A
c	41	41	58.6	18200	4	US-09-949-016-15661	Sequence 15661, A
c	42	41	58.6	19719	4	US-09-949-016-15662	Sequence 15662, A
c	43	41	58.6	19719	4	US-09-949-016-15663	Sequence 15663, A
	44	41	58.6	37895	1	US-08-375-709-1	Sequence 1, Appli
	45	41	58.6	37895	1	US-08-752-929-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-705-771-1
; Sequence 1, Application US/08705771
; Patent No. 6054289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,771
; FILING DATE: August 30, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  550 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-705-771-1

Alignment Scores:
Pred. No.:              0.00135        Length:         550
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     3              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-08-705-771-1 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 2
US-09-417-540-1
; Sequence 1, Application US/09417540
; Patent No. 6639052
;   GENERAL INFORMATION:
;        APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                   Jian Ni and Jing-Shan Hu
;        TITLE OF INVENTION: Human Genes, Sequences and
;                            Expression Products
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                        CECCHI, STEWART & OLSTEIN
;             STREET: 6 BECKER FARM ROAD
;             CITY: ROSELAND
;             STATE: NEW JERSEY
;             COUNTRY: USA
;             ZIP: 07068
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 INCH DISKETTE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: MS-DOS
;             SOFTWARE: WORD PERFECT 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/417,540
;             FILING DATE: 14-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/705,771
;             FILING DATE: August 30, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MULLINS, J.G.
;             REGISTRATION NUMBER: 33,073
;             REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 973-994-1700
;             TELEFAX: 973-994-1744
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 550 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-417-540-1

Alignment Scores:
Pred. No.:              0.00135        Length:         550
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     4              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-417-540-1 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 3
US-09-949-016-1915
; Sequence 1915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1915
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1915

Alignment Scores:
Pred. No.:              0.00178        Length:         702
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     4              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-949-016-1915 (1-702)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        327 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 368

RESULT 4
US-09-949-016-442
; Sequence 442, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 442
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-442
```

```
Alignment Scores:
Pred. No.:              0.00184         Length:         720
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-949-016-442 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 5
US-09-949-016-13657
; Sequence 13657, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13657
;   LENGTH: 8607
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(8607)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13657

Alignment Scores:
Pred. No.:              31.2            Length:         8607
Score:                  53.00           Matches:        10
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  90.91%          Mismatches:     0
Query Match:            75.71%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-949-016-13657 (1-8607)

Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||||
Db       5951 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 5983

RESULT 6
US-09-949-016-12184
; Sequence 12184, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12184
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(8608)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12184

Alignment Scores:
Pred. No.:              31.2            Length:         8608
Score:                  53.00           Matches:        10
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  90.91%          Mismatches:     0
Query Match:            75.71%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-949-016-12184 (1-8608)

Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||||
Db       5951 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 5983

RESULT 7
US-09-489-039A-172/c
; Sequence 172, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 172
;   LENGTH: 825
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-172

Alignment Scores:
Pred. No.:              25              Length:         825
Score:                  47.00           Matches:        9
Percent Similarity:     91.67%          Conservative:   2
Best Local Similarity:  75.00%          Mismatches:     1
Query Match:            67.14%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-489-039A-172 (1-825)

Qy          3 ArgLysGluAspLeuArgProSerAlaProGlnGln 14
              |||   |||||||||||||:::|||||||:::|||
Db        234 CGGATTGAGGATCTCCGCCCCGCTGCGCCACGCCAG 199

RESULT 8
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
```

```
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.:              7.98e+05      Length:          4403765
Score:                  45.00         Matches:         9
Percent Similarity:     78.57%        Conservative:    2
Best Local Similarity:  64.29%        Mismatches:      3
Query Match:            64.29%        Indels:          0
DB:                     3             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-103-840A-2 (1-4403765)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              |||:::|||   |||||||||   ||||||   |||:::|||
Db    3343973 GTGTTGCGTGGCGAGGACCTGCTGCCGTCGACGCCGCGCCAG 3343932

RESULT 9
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.:              7.99e+05      Length:          4411529
Score:                  45.00         Matches:         9
Percent Similarity:     78.57%        Conservative:    2
Best Local Similarity:  64.29%        Mismatches:      3
Query Match:            64.29%        Indels:          0
DB:                     3             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-103-840A-1 (1-4411529)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              |||:::|||   |||||||||   ||||||   |||:::|||
Db    3349641 GTGTTGCGTGGCGAGGACCTGCTGCCGTCGACGCCGCGCCAG 3349600

RESULT 10
US-09-902-540-8804
; Sequence 8804, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8804
;   LENGTH: 1011
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-8804

Alignment Scores:
Pred. No.:              161           Length:          1011
Score:                  43.00         Matches:         7
Percent Similarity:     84.62%        Conservative:    4
Best Local Similarity:  53.85%        Mismatches:      2
Query Match:            61.43%        Indels:          0
DB:                     4             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-902-540-8804 (1-1011)

Qy          2 ValArgLysGluAspLeuArgProSerAlaProGlnGln 14
                ::::||||||   |||:::||||||   ||||||::::::
Db         46 ATGCGCAAGCCCGACGTGCGCCCCGGCGCCCCGGAGCGC 84

RESULT 11
US-08-440-856A-2
; Sequence 2, Application US/08440856A
; Patent No. 5750873
;  GENERAL INFORMATION:
;    APPLICANT:  DELLAPORTA, STEPHEN L.
;    TITLE OF INVENTION:  MATERIALS AND METHODS FOR PRODUCING
;    TITLE OF INVENTION:  PLANTS WITH SINGLE-SEX FLOWERS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 PENNSYLVANIA AVE. N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/440,856A
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLMAN, ROBERT A.
;      REGISTRATION NUMBER:  36,217
;      REFERENCE/DOCKET NUMBER:  05463-20001.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1517
;      TELEFAX:  (202) 887-0763
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1187 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-440-856A-2

Alignment Scores:
Pred. No.:              193           Length:          1187
Score:                  43.00         Matches:         8
Percent Similarity:     78.57%        Conservative:    3
```

```
Best Local Similarity:  57.14%          Mismatches:     3
Query Match:            61.43%          Indels:         0
DB:                     1               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-08-440-856A-2 (1-1187)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              |||||||||:::      :::|||||||   |||||||:::|||
Db        467 GTCGTTCGACGCCGGGGAGTTCGACCGCGTGCTCCGCGTCAA 508

RESULT 12
US-09-902-540-935/c
; Sequence 935, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 935
;   LENGTH: 10096
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(10096)
;   OTHER INFORMATION: unsure at all n locations
US-09-902-540-935

Alignment Scores:
Pred. No.:              2.19e+03        Length:         10096
Score:                  43.00           Matches:        7
Percent Similarity:     84.62%          Conservative:   4
Best Local Similarity:  53.85%          Mismatches:     2
Query Match:            61.43%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-902-540-935 (1-10096)

Qy          2 ValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||   |||:::||||||   ||||||::::::
Db       2820 ATGCGCAAGCCCGACGTGCGCCCCGGCGCCCCGGAGCGC 2782

RESULT 13
US-09-949-016-5443
; Sequence 5443, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5443
;   LENGTH: 689
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5443

Alignment Scores:
Pred. No.:              156             Length:         689
Score:                  42.00           Matches:        8
Percent Similarity:     90.00%          Conservative:   1
Best Local Similarity:  80.00%          Mismatches:     1
Query Match:            60.00%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-949-016-5443 (1-689)

Qy          3 ArgLysGluAspLeuArgProSerAlaPro 12
              |||:::|||   ||||||||||||||||||
Db        156 AGGGAGGAGCAGCTGCGCCCATCAGCTCCC 185

RESULT 14
US-09-419-568F-24
; Sequence 24, Application US/09419568F
; Patent No. 6331613
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fact
;  TITLE OF INVENTION:  (TIFs) The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE: LUD 5543.2
;  CURRENT APPLICATION NUMBER: US/09/419,568F
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US09/354,243
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: US09/178,973
;  PRIOR FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 24
;   LENGTH: 690
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-419-568F-24

Alignment Scores:
Pred. No.:              156             Length:         690
Score:                  42.00           Matches:        8
Percent Similarity:     90.00%          Conservative:   1
Best Local Similarity:  80.00%          Mismatches:     1
Query Match:            60.00%          Indels:         0
DB:                     3               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-419-568F-24 (1-690)

Qy          3 ArgLysGluAspLeuArgProSerAlaPro 12
              |||:::|||   ||||||||||||||||||
Db        157 AGGGAGGAGCAGCTGCGCCCATCAGCTCCC 186

RESULT 15
US-09-354-243B-24
; Sequence 24, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 24
```

; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-24

Alignment Scores:

Pred. No.:	156	Length:	690
Score:	42.00	Matches:	8
Percent Similarity:	90.00%	Conservative:	1
Best Local Similarity:	80.00%	Mismatches:	1
Query Match:	60.00%	Indels:	0
DB:	3	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-354-243B-24 (1-690)

```
Qy          3 ArgLysGluAspLeuArgProSerAlaPro 12
              |||:::|||   ||||||||||||||||||
Db        157 AGGGAGGAGCAGCTGCGCCCATCAGCTCCC 186
```

Search completed: May 4, 2005, 09:42:48
Job time : 667.416 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:52 ; Search time 102.322 Seconds
(without alignments)
809.955 Million cell updates/sec

Title: US-09-017-715A-2_COPY_94_107
Perfect score: 70
Sequence: 1 VVRKEDLRPSAPQQ 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100743_25600/app_query.fasta_1.661
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_@CGN_1_1_703_@runat_04052005_100743_25600 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70	100.0	479	9	ACH15493	Ach15493 Human adu
2	70	100.0	488	12	ADM66887	Adm66887 Human hom
3	70	100.0	550	2	AAV42669	Aav42669 Human bre
4	70	100.0	550	3	AAA39470	Aaa39470 Human HBG
5	70	100.0	550	6	ABL63343	Abl63343 Breast ca
6	70	100.0	550	6	ABV73813	Abv73813 Human gam
7	70	100.0	550	6	ABV73915	Abv73915 Human gam
8	70	100.0	550	10	AAD63568	Aad63568 Human amy
9	70	100.0	550	10	ADG47636	Adg47636 Human amy
10	70	100.0	720	2	AAX29997	Aax29997 Human per
11	70	100.0	720	6	ABS76519	Abs76519 cDNA enco
12	70	100.0	720	10	ADE43864	Ade43864 Human SNC
13	70	100.0	720	12	ADH54342	Adh54342 Human SNC
14	70	100.0	783	4	AAI93778	Aai93778 Human pol
15	70	100.0	796	3	AAF21784	Aaf21784 Human bre
16	70	100.0	990	13	ADR98806	Adr98806 Lung spec
17	54	77.1	677	2	AAX04876	Aax04876 Human gam
18	53	75.7	478	3	AAF21785	Aaf21785 Human bre
19	53	75.7	4606	6	ABT10161	Abt10161 Human bre
20	53	75.7	5666	10	ADE43467	Ade43467 Human SNC
21	53	75.7	5666	10	ADE43468	Ade43468 Polymorph
22	53	75.7	5666	12	ADH53945	Adh53945 Human SNC
23	53	75.7	5666	12	ADH53946	Adh53946 Human IDE
24	53	75.7	6012	10	ADE43314	Ade43314 Human SNC
25	53	75.7	6012	12	ADH54356	Adh54356 Human SNC
26	49	70.0	787	2	AAT51183	Aat51183 Human bre
c 27	48	68.6	135638	10	ABX34289	Abx34289 S. atrool
c 28	47	67.1	657	8	ACA35809	Aca35809 Prokaryot
29	47	67.1	727	2	AAX29998	Aax29998 Mouse per
30	47	67.1	727	12	ADM66886	Adm66886 Murine ad
c 31	47	67.1	825	11	ACH94377	Ach94377 Klebsiell
c 32	45	64.3	429	8	ACA01712	Aca01712 C. glutam
c 33	45	64.3	465	4	AAI16026	Aai16026 Probe #59
c 34	45	64.3	465	4	ABA58473	Aba58473 Human foe
c 35	45	64.3	465	4	AAI38127	Aai38127 Probe #68
c 36	45	64.3	465	4	ABA27546	Aba27546 Probe #60
c 37	45	64.3	465	4	AAK32274	Aak32274 Human bon
c 38	45	64.3	465	4	AAK06585	Aak06585 Human bra
c 39	45	64.3	465	4	ABS31980	Abs31980 Human liv
c 40	45	64.3	465	6	ABS07052	Abs07052 Human gen
41	45	64.3	1410	8	ACA37685	Aca37685 Prokaryot
42	45	64.3	1435	8	ACA38395	Aca38395 Prokaryot
43	45	64.3	1473	8	ACA40765	Aca40765 Prokaryot
44	45	64.3	1488	5	AAH66390	Aah66390 C glutami
45	45	64.3	1491	8	ACA29667	Aca29667 Prokaryot

ALIGNMENTS

RESULT 1
ACH15493
ID ACH15493 standard; cDNA; 479 BP.
XX
AC ACH15493;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult brain cDNA #2705.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 2705; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 479 BP; 120 A; 118 C; 178 G; 56 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	0.00451	Length:	479
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x ACH15493 (1-479)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        293 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 334
```

RESULT 2
ADM66887
ID ADM66887 standard; DNA; 488 BP.
XX
AC ADM66887;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human homologue of murine adipocyte specific gamma synuclein DNA Seq 20.
XX
KW human; adipocyte specific; gene; ds; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; gamma synuclein.
XX
OS Homo sapiens.
XX
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGE-) HMGENE INC.
XX

PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR WPI; 2004-143846/14.
DR P-PSDB; ADM67167.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Claim 11; SEQ ID NO 20; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polynucleotide sequence is a human homologue
CC of a murine adipocyte specific DNA sequence of the invention.
XX
SQ Sequence 488 BP; 127 A; 119 C; 176 G; 66 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.0046	Length:	488
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x ADM66887 (1-488)

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Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332
```

RESULT 3
AAV42669
ID AAV42669 standard; cDNA; 550 BP.
XX
AC AAV42669;
XX
DT 09-NOV-1998 (first entry)
XX
DE Human breast cancer specific gene 1 (BCSG1) cDNA.
XX
KW Breast cancer specific gene 1; BCGS1; human; metastasis; diagnosis;
KW therapy; genetic marker; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12. .395
FT /*tag= a
XX
PN WO9833915-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US001804.
XX
PR 03-FEB-1997; 97US-0037080P.

```
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ji H,  Rosen CA;
XX
DR   WPI; 1998-446811/38.
DR   P-PSDB; AAW63123.
XX
PT   New isolated human breast cancer specific gene - used to develop products
PT   for the diagnosis, clinical management and treatment of breast cancer and
PT   metastases.
XX
PS   Claim 4; Fig 1; 73pp; English.
XX
CC   This cDNA clone corresponds to the transcript of the newly identified
CC   human breast cancer specific gene 1 (BCSG1), and includes an open reading
CC   frame for a 14.2 kDa protein (see AAW63123). It was isolated from a
CC   breast cancer cDNA library following an EST search for novel genes
CC   differentially expressed in breast cancer versus healthy breast tissue.
CC   The clone is deposited at ATCC 97175 and ATCC 97856. A gradient and stage
CC   -specific BCSG1 expression has been demonstrated from virtually no
CC   detectable expression in normal or benign breast to low level and partial
CC   expression in low grade in situ breast carcinoma and high expression in
CC   infiltrating malignant breast carcinomas. BCSG1 is useful as a breast
CC   cancer progression marker. Recombinant vectors and host cells useful for
CC   recombinant production of BCSG1 polypeptides (including epitope- bearing
CC   polypeptides) are provided. BCSG1 polynucleotides, polypeptides and
CC   antibodies can be used for the detection of breast cancer cells or breast
CC   cancer metastasis, and to develop methods for the clinical management and
CC   treatment of breast cancer
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.00526         Length:         550
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x AAV42669 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 4
AAA39470
ID   AAA39470 standard; DNA; 550 BP.
XX
AC   AAA39470;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Human HBGBA67A DNA.
XX
KW   Human; ADA2; cytostatic; gene therapy; treatment; cancer;
KW   amyloid-like protein; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "HBGBA67"
XX
PN   US6054289-A.
XX
PD   25-APR-2000.
XX
PF   30-AUG-1996;   96US-00705771.
XX
PR   30-AUG-1995;   95US-0002993P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA;
XX
DR   WPI; 2000-338491/29.
DR   P-PSDB; AAY87779.
XX
PT   New polynucleotide encoding human AD2 is useful for treating cancer and
PT   for isolating cDNAs and genes having similar biological activity.
XX
PS   Disclosure; Col 27-28; 54pp; English.
XX
CC   This invention describes a novel polynucleotide (I) encoding human ADA2.
CC   The products of the invention have cytostatic activity and can be used
CC   for gene therapy. (I) is useful for treating cancer; as primers and
CC   probes for isolating full length cDNA and genes having similar biological
CC   activity. This sequence encodes a polypeptide derived from the human
CC   HBGBA67X clone which is an amyloid-like protein found in breast tissue
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.00526         Length:         550
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x AAA39470 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 5
ABL63343
ID   ABL63343 standard; DNA; 550 BP.
XX
AC   ABL63343;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Breast cancer related gene sequence SEQ ID NO:1680.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
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PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 1680; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.00526	Length:	550
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x ABL63343 (1-550)

Qy 1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
||||||||||||||||||||||||||||||
Db 291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 6
ABV73813
ID ABV73813 standard; cDNA; 550 BP.
XX
AC ABV73813;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human gamma-synuclein Glu110 variant gene.
XX
KW Gamma-synuclein; human; single nucleotide polymorphism; SNP;
KW schizophrenia; neuroleptic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12. .395
FT /*tag= a
FT /product= "Gamma-synuclein"
FT /transl_except= (pos:213. .215,aa:Glu)
FT variation replace(340,T)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
XX
PN WO200275317-A2.
XX
PD 26-SEP-2002.
XX
PF 14-MAR-2002; 2002WO-EP002872.
XX
PR 15-MAR-2001; 2001US-0276306P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Roberts RC, Van Oostrum J, Voshol J, Tamminga CA;
XX
DR WPI; 2002-750574/81.
DR P-PSDB; ABP54932.
XX
PT Screening for compounds for treating or interfering with the onset of
PT Schizophrenia Spectrum Disorders, by detecting interactions of candidate
PT compounds with the gamma-synuclein polypeptide.
XX
PS Disclosure; Fig 1; 32pp; English.
XX
CC The present sequence is that of cDNA encoding the Glu-110 isoform of
CC human gamma-synuclein. The invention relates to an isoform of gamma-
CC synuclein that is caused by an A/T single nucleotide polymorphism (SNP)
CC at position 329 of the gamma-synuclein coding sequence. This SNP causes a
CC glutamic acid to valine change at amino acid position 110 of gamma-
CC synuclein, and is associated with an increased susceptibility of
CC individuals to schizophrenia spectrum disorders (SSDs). This is the first
CC time that a genetic component of SSDs has been identified, and provides a
CC potential target for diagnosis and treatment of schizophrenia. Gamma-
CC synuclein polypeptides, especially those containing the E110V mutation,
CC are used in a claimed method of screening for compounds useful for the
CC treatment of SSDs, and gamma-synuclein expressing cells are used in a
CC claimed method of screening for agonist or antagonist compounds. An
CC oligonucleotide complementary to part of the gamma-synuclein coding
CC sequence is used for the discrimination of an SNP at position 329 of the
CC coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
CC useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR
CC amplification of a polynucleotide encoding gamma-synuclein and analysis
CC of the occurrence of the SNP at position 329. A transgenic animal useful
CC for the study of SSDs is also claimed
XX
SQ Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.:              0.00526        Length:         550
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x ABV73813 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 7
ABV73915
ID   ABV73915 standard; cDNA; 550 BP.
XX
AC   ABV73915;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human gamma-synuclein Val110 variant gene.
XX
KW   Gamma-synuclein; human; single nucleotide polymorphism; SNP;
KW   schizophrenia; neuroleptic; mutant; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "Gamma-synuclein"
FT                   /transl_except= (pos:213. .215,aa:Glu)
FT   variation       replace(340,A)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200275317-A2.
XX
PD   26-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-EP002872.
XX
PR   15-MAR-2001; 2001US-0276306P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Roberts RC,  Van Oostrum J,  Voshol J,  Tamminga CA;
XX
DR   WPI; 2002-750574/81.
DR   P-PSDB; ABP54933.
XX
PT   Screening for compounds for treating or interfering with the onset of
PT   Schizophrenia Spectrum Disorders, by detecting interactions of candidate
PT   compounds with the gamma-synuclein polypeptide.
XX
PS   Disclosure; Page; 32pp; English.
XX
CC   The present sequence is that of cDNA encoding the Val-110 isoform of
CC   human gamma-synuclein. The invention relates to an isoform of gamma-
CC   synuclein that is caused by an A/T single nucleotide polymorphism (SNP)
CC   at position 329 of the gamma-synuclein coding sequence. This SNP causes a
CC   glutamic acid to valine change at amino acid position 110 of gamma-
CC   synuclein, and is associated with an increased susceptibility of
CC   individuals to schizophrenia spectrum disorders (SSDs). This is the first
CC   time that a genetic component of SSDs has been identified, and provides a
CC   potential target for diagnosis and treatment of schizophrenia. Gamma-
CC   synuclein polypeptides, especially those containing the E110V mutation,
CC   are used in a claimed method of screening for compounds useful for the
CC   treatment of SSDs, and gamma-synuclein expressing cells are used in a
CC   claimed method of screening for agonist or antagonist compounds. An
CC   oligonucleotide complementary to part of the gamma-synuclein coding
CC   sequence is used for the discrimination of an SNP at position 329 of the
CC   coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
CC   useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR
CC   amplification of a polynucleotide encoding gamma-synuclein and analysis
CC   of the occurrence of the SNP at position 329. A transgenic animal useful
CC   for the study of SSDs is also claimed. Note: The present sequence is not
CC   shown in the specification but is derived from the gamma-synuclein
CC   sequence given in Fig 1 (see ABV73813)
XX
SQ   Sequence 550 BP; 131 A; 145 C; 192 G; 82 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.00526        Length:         550
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x ABV73915 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 8
AAD63568
ID   AAD63568 standard; cDNA; 550 BP.
XX
AC   AAD63568;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human amyloid-like protein cDNA.
XX
KW   Human; genetic disease; muscular dystrophy; cystic fibrosis; cytostatic;
KW   scientific research; gene therapy; gene; amyloid-like protein; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "Human amyloid-like protein"
XX
PN   US6639052-B1.
XX
PD   28-OCT-2003.
XX
PF   14-OCT-1999;   99US-00417540.
XX
PR   30-AUG-1995;   95US-0002993P.
PR   30-AUG-1996;   96US-00705771.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA;
XX
DR   WPI; 2003-842790/78.
DR   P-PSDB; ABW02024.
XX
PT   New isolated protein and nucleic acid molecules, useful for diagnostic
PT   and therapeutic purposes, e.g. for treating genetic diseases such as
PT   muscular dystrophy or cystic fibrosis.
XX
PS   Example 5; Fig 1; 0pp; English.
XX
CC   The invention relates to isolated new isolated protein and nucleic acid
CC   molecules useful for diagnostic and therapeutic purposes. The invention
CC   is for treating genetic diseases such as muscular dystrophy or cystic
```

```
CC   fibrosis, and for in vitro purposes related to scientific research,
CC   synthesis of DNA and manufacture of DNA vectors. The invention is useful
CC   in gene therapy. The present sequence is human amyloid-like protein cDNA
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.00526       Length:        550
Score:                  70.00         Matches:       14
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     10            Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AAD63568 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 9
ADG47636
ID   ADG47636 standard; cDNA; 550 BP.
XX
AC   ADG47636;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human amyloid like protein cDNA.
XX
KW   ss; gene; muscular dystrophy; cystic fibrosis; hypertension;
KW   angina pectoris; myocardial infarction; ulcer; asthma; allergy;
KW   psychosis; depression; migraine; vomiting; benign prostatic hypertrophy;
KW   osteoporosis; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "Amyloid like protein"
XX
PN   US2003208043-A1.
XX
PD   06-NOV-2003.
XX
PF   04-JUN-2003; 2003US-00453478.
XX
PR   30-AUG-1995;   95US-0002993P.
PR   30-AUG-1996;   96US-00705771.
PR   14-OCT-1999;   99US-00417540.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA,  Gentz RL,  Ji H,  Ni J,  Hu J;
XX
DR   WPI; 2003-864796/80.
DR   P-PSDB; ADG47647.
XX
PT   New human polypeptides and polynucleotides, useful for diagnosing or
PT   treating genetic diseases such as muscular dystrophy or cystic fibrosis,
PT   hypertension, asthma, depression or osteoporosis.
XX
PS   Claim 18; SEQ ID NO 1; 56pp; English.
XX
CC   The invention relates to an isolated human polypeptide. The polypeptides,
CC   polynucleotides, agonists or antagonist are useful for diagnosing or
CC   treating genetic diseases such as muscular dystrophy or cystic fibrosis,
CC   hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
CC   allergies, psychoses, depression, migraine, vomiting, benign prostatic
CC   hypertrophy or osteoporosis. The polypeptides and polynucleotides are
CC   useful for in vitro purposes related to scientific research, synthesis of
CC   DNA and manufacture of DNA vector. The present sequence represents cDNA
CC   encoding human amyloid like protein.
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.00526       Length:        550
Score:                  70.00         Matches:       14
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     10            Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x ADG47636 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 10
AAX29997
ID   AAX29997 standard; DNA; 720 BP.
XX
AC   AAX29997;
XX
DT   06-JUL-1999  (first entry)
XX
DE   Human persyn gene.
XX
KW   Human; synuclein; persyn; diagnosis; neurodegenerative disorder; cancer;
KW   breast; skin; intermediate filament damage; ss.
XX
OS   Homo sapiens.
XX
PN   EP908727-A1.
XX
PD   14-APR-1999.
XX
PF   21-SEP-1998;   98EP-00307628.
XX
PR   19-SEP-1997;   97GB-00019879.
XX
PA   (NEUR-) NEUROPA LTD.
PA   (UYSA-) UNIV ST ANDREWS.
XX
DR   WPI; 1999-217169/19.
DR   P-PSDB; AAY07271.
XX
PT   New synuclein protein (persyn) and gene, useful in assays for screening,
PT   diagnosing or monitoring cancer, neurodegenerative disorders or skin
PT   disorders.
XX
PS   Claim 29; Page 16-17; 39pp; English.
XX
CC   This sequence represents the gene encoding a novel human synuclein family
CC   member designated persyn. The sequence is useful for screening,
CC   diagnosing or monitoring cancer (especially breast or skin cancer),
CC   neurodegenerative disorders or skin disorders and for identifying cells
CC   having intermediate filament damage
XX
SQ   Sequence 720 BP; 173 A; 209 C; 215 G; 123 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.00711       Length:        720
Score:                  70.00         Matches:       14
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     2             Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AAX29997 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
```

```
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 11
ABS76519
ID   ABS76519 standard; cDNA; 720 BP.
XX
AC   ABS76519;
XX
DT   11-DEC-2002  (first entry)
XX
DE   cDNA encoding human ovarian cancer marker OV60.
XX
KW   Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW   central nervous system disorder; bacterial meningitis; viral meningitis;
KW   Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW   brain herniation; inflammation; encephalitis; testicular disorder;
KW   nontuberculous granulomatous orchitis; connective tissue disorder;
KW   heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW   histological type; carcinogenic; ovarian cancer marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200271928-A2.
XX
PD   19-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-US007826.
XX
PR   14-MAR-2001; 2001US-0276025P.
PR   14-MAR-2001; 2001US-0276026P.
PR   10-AUG-2001; 2001US-0311732P.
PR   19-SEP-2001; 2001US-0323580P.
PR   26-SEP-2001; 2001US-0324967P.
PR   26-SEP-2001; 2001US-0325102P.
PR   26-SEP-2001; 2001US-0325149P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI   Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
PI   Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX
DR   WPI; 2002-723277/78.
DR   P-PSDB; ABG96420.
XX
PT   Assessing whether a patient is afflicted with ovarian cancer, useful in
PT   assessing the stage or progression of the disease, comprises comparing
PT   the expression level of a cancer marker in a sample from a patient and
PT   from a non cancer patient.
XX
PS   Disclosure; Page 411; 481pp; English.
XX
CC   The present invention relates to a new method for assessing whether a
CC   patient is afflicted with ovarian cancer. The method involves comparing
CC   the expression level of a marker in a patient sample and the normal level
CC   of expression of the marker in a control non-ovarian cancer sample, where
CC   the marker is selected from 363 cancer markers described in the
CC   specification. The method of the invention is useful in diagnosing or
CC   characterising cancer, in detecting the presence of cancer as early as
CC   possible, and the recurrence of ovarian cancer. The method may also be of
CC   particular use with patients having an enhanced risk of developing
CC   ovarian cancer (e.g. patients having a familial history of ovarian
CC   cancer). The cancer markers may be used in the management and treatment
CC   of e.g. brain and central nervous system disorders (e.g. bacterial and
CC   viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC   disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
CC   inflammations (e.g. bacterial or viral meningitis or encephalitis),
CC   testicular disorders (e.g. nontuberculous granulomatous orchitis),
CC   connective tissue disorders, or heart disorders (e.g. ischaemic heart
CC   disease or atherosclerosis). The compositions and methods may also be
CC   used in assessing the histological type of neoplasm associated with
CC   ovarian cancer, monitoring the progression of ovarian cancer, determining
CC   whether ovarian cancer has metastasized or is likely to metastasize,
CC   selecting a composition for inhibiting ovarian cancer, assessing the
CC   ovarian carcinogenic potential of a compound, or inhibiting ovarian
CC   cancer or at risk of developing ovarian cancer. The present nucleic acid
CC   sequence encodes one of the ovarian cancer markers described in the
CC   invention
XX
SQ   Sequence 720 BP; 173 A; 209 C; 215 G; 123 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.00711        Length:          720
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x ABS76519 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 12
ADE43864
ID   ADE43864 standard; cDNA; 720 BP.
XX
AC   ADE43864;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human SNCG cDNA, SEQ ID 469.
XX
KW   Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW   Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW   Chromosome 10; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003054143-A2.
XX
PD   03-JUL-2003.
XX
PF   25-OCT-2002; 2002WO-US034679.
XX
PR   25-OCT-2001; 2001US-0339525P.
PR   08-NOV-2001; 2001US-0336929P.
PR   08-NOV-2001; 2001US-0338010P.
PR   09-NOV-2001; 2001US-0338363P.
PR   04-DEC-2001; 2001US-0337052P.
PR   28-MAR-2002; 2002US-0368919P.
XX
PA   (NEUR-) NEUROGENETICS INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI   Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR   WPI; 2003-559131/52.
XX
PT   Determining a predisposition for or the occurrence of neurodegenerative
PT   disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT   the presence or absence of an allelic variant of one or more polymorphic
PT   regions.
XX
PS   Claim 84; Page 740; 848pp; English.
XX
CC   The present invention relates to a method (M1) for determining a
CC   predisposition for or the occurrence of neurodegenerative disease in a
CC   subject. The method comprises detecting in a target nucleic acid obtained
CC   from the subject the presence or absence of an allelic variant of one or
CC   more polymorphic regions of one or more genes selected from uPA
CC   (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC   degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
```

CC lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC presence of at least one of the allelic variant of one or more
CC polymorphic regions is indicative of a predisposition for or the
CC occurrence of neurodegenerative disease. The genes are all located on
CC chromosome 10. M1 is useful for determining a predisposition for or the
CC occurrence of, and for treating neurodegenerative disease, particularly
CC Alzheimer's disease.
XX
SQ Sequence 720 BP; 172 A; 205 C; 212 G; 120 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.:	0.00711	Length:	720
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x ADE43864 (1-720)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369
```

RESULT 13
ADH54342
ID ADH54342 standard; cDNA; 720 BP.
XX
AC ADH54342;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human SNCG gene cDNA sequence SeqID469.
XX
KW human; neurodegenerative disease; urokinase plasminogen activator; uPA;
KW gamma-synuclein; SNCG; insulin degrading enzyme; IDE;
KW kinesin-like protein 1; KNSL1; lysosomal acid lipase; LIPA;
KW tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; ss.
XX
OS Homo sapiens.
XX
PN US2003224380-A1.
XX
PD 04-DEC-2003.
XX
PF 25-OCT-2002; 2002US-00282174.
XX
PR 25-OCT-2001; 2001US-0339525P.
PR 25-OCT-2001; 2001US-0348065P.
PR 02-NOV-2001; 2001US-0336983P.
PR 08-NOV-2001; 2001US-0336929P.
PR 08-NOV-2001; 2001US-0338010P.
PR 09-NOV-2001; 2001US-0338363P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Becker KD, Velicelebi G, Ellliott KJ, Wang X, Tanzi RE;
PI Bertram L, Saunders AJ, Mullin KM, Sampson AJ;
XX
DR WPI; 2004-060538/06.
XX
PT Determining a predisposition for or the occurrence of neurodegenerative
PT disease, particularly Alzheimer's disease, comprises determining the
PT presence of a polymorphism in the uPA, SNCG, IDE, KNSL1, LIPA or TNFRSF6
PT gene.
XX
PS Claim 84; SEQ ID NO 469; 205pp; English.
XX
CC This invention relates to a novel method of determining a predisposition
CC for or the occurrence of neurodegenerative disease comprising detecting
CC in a target nucleic acid obtained from the subject the presence of an

CC allelic variant of polymorphic regions of human genes selected from
CC urokinase plasminogen activator (uPA), gamma-synuclein (SNCG), insulin
CC degrading enzyme (IDE), kinesin-like protein 1 (KNSL1), lysosomal acid
CC lipase (LIPA) and tumour necrosis factor receptor SF6 (TNFRSF6). The
CC method is useful in determining the presence or predisposition to a
CC neurodegenerative disease, particularly Alzheimer's disease. The present
CC sequence is the cDNA sequence of the human SNCG gene which is related to
CC the invention.
XX
SQ Sequence 720 BP; 172 A; 205 C; 212 G; 120 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.:	0.00711	Length:	720
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x ADH54342 (1-720)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369
```

RESULT 14
AAI93778
ID AAI93778 standard; cDNA; 783 BP.
XX
AC AAI93778;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 13838.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR P-PSDB; AAO13847.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 1; SEQ ID NO 13838; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 783 BP; 187 A; 232 C; 237 G; 127 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.0078	Length:	783
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x AAI93778 (1-783)

```
Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        393 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 434
```

RESULT 15
AAF21784
ID AAF21784 standard; DNA; 796 BP.
XX
AC AAF21784;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 171.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS Homo sapiens.
XX
PN WO200055173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005881.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-611515/58.
DR P-PSDB; AAB58881.
XX
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention, treatment
PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT neurological diseases.
XX
PS Claim 1; Page 608; 1299pp; English.
XX
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC protein sequences are used in the diagnosis of cancer, particularly
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC and agonists may also be used in the diagnosis, prevention and treatment
CC of immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC cardiovascular disorders such as myocardial ischaemias; wound healing;
CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases
XX
SQ Sequence 796 BP; 195 A; 233 C; 240 G; 126 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	0.00795	Length:	796
Score:	70.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-017-715A-2_COPY_94_107 (1-14) x AAF21784 (1-796)

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Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
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Db        388 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 429
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Search completed: May 4, 2005, 09:26:19
Job time : 105.322 secs

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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:55 ; Search time 795.087 Seconds
(without alignments)
853.206 Million cell updates/sec

Title: US-09-017-715A-2_COPY_94_107
Perfect score: 70
Sequence: 1 VVRKEDLRPSAPQQ 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_htg:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70	100.0	381	9	CR541790	CR541790 Homo sapi
2	70	100.0	384	9	CR541788	CR541788 Homo sapi
3	70	100.0	488	9	AF411524	AF411524 Homo sapi
4	70	100.0	550	6	AR412236	AR412236 Sequence
5	70	100.0	550	6	AX331171	AX331171 Sequence
6	70	100.0	550	6	BD022727	BD022727 Mammary c
7	70	100.0	550	9	AF010126	AF010126 Homo sapi
8	70	100.0	704	6	CQ720882	CQ720882 Sequence
9	70	100.0	720	6	E36333	E36333 Analytical
10	70	100.0	720	6	AX004527	AX004527 Sequence
11	70	100.0	720	9	AF017256	AF017256 Homo sapi
12	70	100.0	738	11	BV177827	BV177827 sqnm97020
13	70	100.0	758	9	BC014098	BC014098 Homo sapi
14	53	75.7	4606	9	AF044311	AF044311 Homo sapi
15	53	75.7	5491	9	AF037207	AF037207 Homo sapi
c 16	53	75.7	149668	9	AC025268	AC025268 Homo sapi
c 17	53	75.7	175542	2	AC150062	AC150062 Gallus ga
18	53	75.7	188771	2	AC150073	AC150073 Gallus ga
c 19	53	75.7	190496	2	BX510354	BX510354 Homo sapi
c 20	49	70.0	168860	9	AL160175	AL160175 Human DNA
21	49	70.0	219205	10	AL611985	AL611985 Mouse DNA
c 22	48	68.6	135638	1	AF484556	AF484556 Streptomy
23	48	68.6	211075	10	AC128668	AC128668 Mus muscu
24	48	68.6	242974	2	AC103570	AC103570 Rattus no
25	47	67.1	488	10	AY518351	AY518351 Rattus no
26	47	67.1	727	6	E36334	E36334 Analytical
27	47	67.1	727	6	AX004529	AX004529 Sequence
28	47	67.1	727	10	AF017255	AF017255 Mus muscu
29	47	67.1	732	10	RNSDSYNGE	X86789 R.norvegicu
30	47	67.1	748	10	BC028508	BC028508 Mus muscu
31	47	67.1	788	5	BC075925	BC075925 Danio rer
c 32	47	67.1	825	6	AR383443	AR383443 Sequence
33	47	67.1	1252	3	AK114896	AK114896 Ciona int
34	47	67.1	1646	3	AK114539	AK114539 Ciona int
c 35	47	67.1	191707	2	CR847971	CR847971 Danio rer
c 36	47	67.1	247309	2	AC097837	AC097837 Rattus no
37	46	65.7	154356	10	AC131119	AC131119 Mus muscu
c 38	46	65.7	172435	8	OSJN00163	AL662963 Oryza sat
39	46	65.7	189771	2	AC118514	AC118514 Rattus no
40	46	65.7	246005	2	AC095834	AC095834 Rattus no
41	46	65.7	286756	1	AP000990	AP000990 Sulfolobu
c 42	45	64.3	465	6	CQ070159	CQ070159 Sequence
c 43	45	64.3	465	6	CQ097954	CQ097954 Sequence
c 44	45	64.3	465	6	CQ136809	CQ136809 Sequence
c 45	45	64.3	465	6	CQ174616	CQ174616 Sequence

ALIGNMENTS

RESULT 1
CR541790
LOCUS CR541790 381 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPDo834B0231D for gene SNCG, synuclein, gamma (breast cancer-specific protein 1); complete cds, without stopcodon.
ACCESSION CR541790
VERSION CR541790.1 GI:49456536
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 381)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 381)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

```
COMMENT     RZPD; RZPDo834B0231D, ORFNo 3631
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834B0231D RZPDLIB;
            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            Clone name at Harvard Institute of Proteomics
            (www.hip.harvard.edu): FLH130940.01L
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned without stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence BC014098
            we did not find any amino acid exchanges.
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES              Location/Qualifiers
     source           1. .381
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="RZPDo834B0231D"
                      /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                      /lab_host="DH5Alpha"
                      /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene             1. .381
                      /gene="SNCG"
     CDS              1. .>381
                      /gene="SNCG"
                      /codon_start=1
                      /protein_id="CAG46589.1"
                      /db_xref="GI:49456537"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              0.00392       Length:          381
Score:                  70.00         Matches:         14
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     9             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x CR541790 (1-381)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
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Db        280 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 321

RESULT 2
CR541788
LOCUS       CR541788                384 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens full open reading frame cDNA clone RZPDo834F0930D for
            gene SNCG, synuclein, gamma (breast cancer-specific protein 1);
            complete cds, incl. stopcodon.
ACCESSION   CR541788
VERSION     CR541788.1  GI:49456532
KEYWORDS    Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Cloning of human full open reading frames in Gateway(TM) system
            entry vector (pDONR201)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 384)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
            Germany
COMMENT     RZPD; RZPDo834F0930D, ORFNo 3605
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834F0930D RZPDLIB;
            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            Clone name at Harvard Institute of Proteomics
            (www.hip.harvard.edu): FLH131021.01X
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned incl. stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence BC014098
            we did not find any amino acid exchanges.
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES              Location/Qualifiers
     source           1. .384
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="RZPDo834F0930D"
                      /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                      /lab_host="DH5Alpha"
                      /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene             1. .384
                      /gene="SNCG"
     CDS              1. .384
                      /gene="SNCG"
                      /codon_start=1
                      /protein_id="CAG46587.1"
                      /db_xref="GI:49456533"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              0.00395       Length:          384
Score:                  70.00         Matches:         14
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Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
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DB:                    9             Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x CR541788 (1-384)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        280 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 321

RESULT 3
AF411524
LOCUS       AF411524                488 bp    mRNA    linear   PRI 20-SEP-2001
DEFINITION  Homo sapiens synuclein gamma mRNA, complete cds.
ACCESSION   AF411524
VERSION     AF411524.1  GI:15705904
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Han,C., Zhang,B., Peng,X., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2001) Department of Biochemistry, Institute of
            Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong
            Dan San Tiao, Beijing 100005, P.R. China
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             12. .395
                     /note="SNCG; breast cancer-specific protein 1"
                     /codon_start=1
                     /product="synuclein gamma"
                     /protein_id="AAL05870.1"
                     /db_xref="GI:15705905"
                     /translation="MDVFKKGFSIAKEGVVDAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              0.00488       Length:        488
Score:                  70.00         Matches:       14
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     9             Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AF411524 (1-488)

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Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 4
AR412236
LOCUS       AR412236                550 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6639052.
ACCESSION   AR412236
VERSION     AR412236.1  GI:40167022
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Moore,P.A.
  TITLE     Human ADA2 polypeptides
  JOURNAL   Patent: US 6639052-A 1 28-OCT-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN

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Score:                  70.00         Matches:       14
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AR412236 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 5
AX331171
LOCUS       AX331171                550 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 1680 from Patent WO0194629.
ACCESSION   AX331171
VERSION     AX331171.1  GI:18121805
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 1680 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .550
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                     /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.:              0.00543       Length:        550
Score:                  70.00         Matches:       14
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-09-017-715A-2_COPY_94_107 (1-14) x AX331171 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 6
BD022727
LOCUS       BD022727                550 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Mammary cancer-specific gene 1.
ACCESSION   BD022727
VERSION     BD022727.1  GI:22563950
KEYWORDS    JP 2001509664-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Ji,H. and Rosen,C.A.
  TITLE     Mammary cancer-specific gene 1
  JOURNAL   Patent: JP 2001509664-A 1 24-JUL-2001;
            HUMAN GENOME SCIENCES INC
COMMENT     PN   JP 2001509664-A/1
            PD   24-JUL-2001
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            PF   03-FEB-1998 JP 1998515053
            PR   03-FEB-1997 US    60/037080
            PI   HONGJUN JI,CRAIG A ROSEN
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68,G01N33/574,C12N15/00,C12N5/00 CC
            Strandedness: Double;
            CC   Topology: Both;
            FH   Key             Location/Qualifiers
            FT   CDS             12. .392.
FEATURES              Location/Qualifiers
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                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0.00543        Length:         550
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x BD022727 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 7
AF010126
LOCUS       AF010126                550 bp    mRNA    linear   PRI 26-JUL-1997
DEFINITION  Homo sapiens breast cancer-specific protein 1 (BCSG1) mRNA,
            complete cds.
ACCESSION   AF010126
VERSION     AF010126.1  GI:2281473
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K.,
            Rosen,C. and Shi,Y.E.
  TITLE     Identification of a breast cancer-specific gene, BCSG1, by direct
            differential cDNA sequencing
  JOURNAL   Cancer Res. 57 (4), 759-764 (1997)
  MEDLINE   97178957
   PUBMED   9044857
REFERENCE   2  (bases 1 to 550)
  AUTHORS   Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K.,
            Rosen,C. and Shi,Y.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUN-1997) Ped. Res., Long Island Jewish Medical
            Center, 270-05 76th Ave., New Hyde Park, NY 11040, USA
FEATURES              Location/Qualifiers
     source           1. .550
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="breast cancer"
                      /note="cDNA highly abundant in a breast cancer library but
                      not in normal library"
     gene             1. .550
                      /gene="BCSG1"
     CDS              12. .395
                      /gene="BCSG1"
                      /note="breast cancer-specific protein 1; synuclein-like;
                      AD amyloid-like"
                      /codon_start=1
                      /product="BCSG1 protein"
                      /protein_id="AAB64109.1"
                      /db_xref="GI:2281474"
                      /translation="MDVFKKGFSIAKKGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSKAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              0.00543        Length:         550
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     9              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x AF010126 (1-550)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332

RESULT 8
CQ720882
LOCUS       CQ720882                704 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 6816 from Patent WO02068579.
ACCESSION   CQ720882
VERSION     CQ720882.1  GI:42281739
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 6816 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES              Location/Qualifiers
     source           1. .704
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0.00676        Length:         704
Score:                  70.00          Matches:        14
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x CQ720882 (1-704)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||||
Db        327 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 368

RESULT 9
E36333
LOCUS       E36333                  720 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Analytical matter based on synuclein and novel synuclein protein.
ACCESSION   E36333
VERSION     E36333.1  GI:13022626
KEYWORDS    JP 1999239488-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
```

```
  AUTHORS   Andrew,S.M., Valdimia,R.B. and Arun,M.D.
  TITLE     Analytical matter based on synuclein and novel synuclein protein
  JOURNAL   Patent: JP 1999239488-A 1 07-SEP-1999;
            THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS,NYUROBA LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 1999239488-A/1
            PD   07-SEP-1999
            PF   21-SEP-1998 JP 1998306283
            PR   19-SEP-1997 GB    9719879.0
            PI   ANDREW SMITH MAKKARION,VALDIMIA RUVOVICHI BUCHIMAN, PI   ARUN
            MILWARD DAVIS
            PC   C12N15/09,A01K67/027,C12Q1/68,G01N33/53,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   CDS             (49). .(432).
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0.0069          Length:         720
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x E36333 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 10
AX004527
LOCUS       AX004527                720 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 1 from Patent EP0908727.
ACCESSION   AX004527
VERSION     AX004527.1  GI:9927977
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   .
  TITLE     Synuclein-based assay and synuclein protein
  JOURNAL   Patent: EP 0908727-A 1 14-APR-1999;
            NEUROPA LIMITED (GB); UNIV COURT OF THE UNIVERSITY O (GB)
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
     CDS              49. .432
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAC04899.1"
                      /db_xref="GI:9927978"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGVASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              0.0069          Length:         720
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x AX004527 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 11
AF017256
LOCUS       AF017256                720 bp    mRNA    linear   PRI 23-SEP-1998
DEFINITION  Homo sapiens persyn mRNA, complete cds.
ACCESSION   AF017256
VERSION     AF017256.1  GI:3642774
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ninkina,N.N., Alimova-Kost,M.V., Paterson,J.W., Delaney,L.,
            Cohen,B.B., Imreh,S., Gnuchev,N.V., Davies,A.M. and Buchman,V.L.
  TITLE     Organization, expression and polymorphism of the human persyn gene
  JOURNAL   Hum. Mol. Genet. 7 (9), 1417-1424 (1998)
  MEDLINE   98367030
   PUBMED   9700196
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Buchman,V.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-1997) School of Biomedical Sciences, Univ. of St.
            Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
            Scotland
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
     5'UTR            1. .48
     CDS              49. .432
                      /note="member of the synuclein family with a distinct
                      pattern of expression"
                      /codon_start=1
                      /product="persyn"
                      /protein_id="AAC36550.1"
                      /db_xref="GI:3642775"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGVASKEKEEVAEEAQSGGD"
     3'UTR            433. .720
     polyA_signal     684. .689
     polyA_site       706
ORIGIN

Alignment Scores:
Pred. No.:              0.0069          Length:         720
Score:                  70.00           Matches:        14
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x AF017256 (1-720)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        328 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

RESULT 12
BV177827
LOCUS       BV177827                738 bp    DNA     linear   STS 10-JUN-2004
DEFINITION  sqnm97020 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
            tagged site.
ACCESSION   BV177827
VERSION     BV177827.1  GI:48014020
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```
KEYWORDS    STS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 738)
  AUTHORS   Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
            Cantor,C.R. and Braun,A.
  TITLE     Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
            Regions
  JOURNAL   Genome Res. (2004) In press
COMMENT
            Contact: Andreas Braun
            Pharmaceuticals division
            Sequenom, Inc.
            3595 John Hopkins Court, San Diego, CA 92121, USA
            Tel: 18582029018
            Fax: 18582029020
            Email: abraun@sequenom.com
            Primer A: No primer sequence submitted
            Primer B: No primer sequence submitted
            STS size: 738.
FEATURES             Location/Qualifiers
     source          1. .738
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Human DNA (Sequenom)"
     STS             <1. .>738
ORIGIN

Alignment Scores:
Pred. No.:                0.00705        Length:          738
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       11             Gaps:            0

US-09-017-715A-2_COPY_94_107 (1-14) x BV177827 (1-738)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        330 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 371

RESULT 13
BC014098
LOCUS       BC014098                 758 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens synuclein, gamma (breast cancer-specific protein 1),
            mRNA (cDNA clone MGC:20132 IMAGE:4546444), complete cds.
ACCESSION   BC014098
VERSION     BC014098.2  GI:33878363
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 758)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 19, 2003 this sequence version replaced gi:15559464.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 28 Row: p Column: 20
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4507112.
FEATURES             Location/Qualifiers
     source          1. .758
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:20132 IMAGE:4546444"
                     /tissue_type="Colon, adenocarcinoma"
                     /clone_lib="NIH_MGC_15"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene            1. .758
                     /gene="SNCG"
                     /note="synonyms: SR, BCSG1"
                     /db_xref="LocusID:6623"
                     /db_xref="MIM:602998"
     CDS             71. .454
                     /gene="SNCG"
                     /codon_start=1
                     /product="synuclein, gamma (breast cancer-specific protein
                     1)"
                     /protein_id="AAH14098.1"
                     /db_xref="GI:15559465"
                     /db_xref="LocusID:6623"
                     /db_xref="MIM:602998"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:                0.00722        Length:          758
Score:                    70.00          Matches:         14
Percent Similarity:       100.00%        Conservative:    0
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Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     9              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x BC014098 (1-758)

Qy          1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
              ||||||||||||||||||||||||||||||||||||||||||
Db        350 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 391

RESULT 14
AF044311
LOCUS       AF044311                4606 bp    DNA     linear   PRI 29-JUL-1998
DEFINITION  Homo sapiens gamma-synuclein gene, complete cds.
ACCESSION   AF044311
VERSION     AF044311.1  GI:3347841
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4606)
  AUTHORS   Lavedan,C., Leroy,E., Dehejia,A., Buchholtz,S., Dutra,A.,
            Nussbaum,R.L. and Polymeropoulos,M.H.
  TITLE     Identification, localization and characterization of the human
            gamma-synuclein gene
  JOURNAL   Hum. Genet. 103 (1), 106-112 (1998)
  MEDLINE   98407804
   PUBMED   9737786
REFERENCE   2  (bases 1 to 4606)
  AUTHORS   Lavedan,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1998) NHGRI/LGDR, NIH, 49 Convent Drive,
            Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .4606
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10q23; between markers WI-5226 and AFM225YD12"
     mRNA            join(1. .173,988. .1029,1356. .1483,3953. .4024,4314. .4606)
                     /product="gamma-synuclein"
     5'UTR           1. .52
     CDS             join(53. .173,988. .1029,1356. .1483,3953. .4024,4314. .4334)
                     /codon_start=1
                     /product="gamma-synuclein"
                     /protein_id="AAC27738.1"
                     /db_xref="GI:3347842"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGVASKEKEEVAEEAQSGGD"
     3'UTR           4335. .4606
ORIGIN

Alignment Scores:
Pred. No.:              38.4           Length:         4606
Score:                  53.00          Matches:        10
Percent Similarity:     100.00%        Conservative:   1
Best Local Similarity:  90.91%         Mismatches:     0
Query Match:            75.71%         Indels:         0
DB:                     9              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x AF044311 (1-4606)

Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||
Db       3950 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 3982

RESULT 15
AF037207
LOCUS       AF037207                5491 bp    DNA     linear   PRI 23-SEP-1998
DEFINITION  Homo sapiens persyn gene, complete cds.
ACCESSION   AF037207
VERSION     AF037207.1  GI:3642902
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5491)
  AUTHORS   Ninkina,N.N., Alimova-Kost,M.V., Paterson,J.W., Delaney,L.,
            Cohen,B.B., Imreh,S., Gnuchev,N.V., Davies,A.M. and Buchman,V.L.
  TITLE     Organization, expression and polymorphism of the human persyn gene
  JOURNAL   Hum. Mol. Genet. 7 (9), 1417-1424 (1998)
  MEDLINE   98367030
   PUBMED   9700196
REFERENCE   2  (bases 1 to 5491)
  AUTHORS   Buchman,V.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-1997) Biomedical Sciences, University of St.
            Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
            Scotland, UK
FEATURES             Location/Qualifiers
     source          1. .5491
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10q23.2-q23.3"
     mRNA            join(<567. .729,1544. .1585,1912. .2039,4515. .4586,
                     4876. .>5169)
                     /product="persyn"
     exon            <567. .729
                     /number=1
     CDS             join(609. .729,1544. .1585,1912. .2039,4515. .4586,4876. .4896)
                     /note="member of synuclein family; similar to the Homo
                     sapiens persyn protein encoded by sequence presented in
                     GenBank Accession Number AF017256"
                     /codon_start=1
                     /product="persyn"
                     /protein_id="AAC36586.1"
                     /db_xref="GI:3642903"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGVASKEKEEVAEEAQSGGD"
     exon            1544. .1585
                     /number=2
     exon            1912. .2039
                     /number=3
     exon            4515. .4586
                     /number=4
     misc_difference 4552
                     /note="polymorphism resulting in valine to glutamic acid
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                     /number=5
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                     /note="in human persyn mRNA clone H1 deposited in GenBank
                     Accession Number AF017256"
                     /replace="t"
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ORIGIN

Alignment Scores:
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Score:                  53.00          Matches:        10
Percent Similarity:     100.00%        Conservative:   1
Best Local Similarity:  90.91%         Mismatches:     0
Query Match:            75.71%         Indels:         0
DB:                     9              Gaps:           0

US-09-017-715A-2_COPY_94_107 (1-14) x AF037207 (1-5491)
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Qy          4 LysGluAspLeuArgProSerAlaProGlnGln 14
              :::||||||||||||||||||||||||||||||
Db       4512 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 4544
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Search completed: May 4, 2005, 11:53:27
Job time : 801.421 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:55 ; Search time 454.336 Seconds
(without alignments)
853.206 Million cell updates/sec

Title: US-09-017-715A-2_COPY_120_127
Perfect score: 41
Sequence: 1 EEAQSGGD 8

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: gb_un:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	381	9	CR541790	CR541790 Homo sapi
2	41	100.0	384	9	CR541788	CR541788 Homo sapi
3	41	100.0	488	9	AF411524	AF411524 Homo sapi
4	41	100.0	550	6	AR412236	AR412236 Sequence
5	41	100.0	550	6	AX331171	AX331171 Sequence
6	41	100.0	550	6	BD022727	BD022727 Mammary c
7	41	100.0	550	9	AF010126	AF010126 Homo sapi
8	41	100.0	704	6	CQ720882	CQ720882 Sequence
9	41	100.0	720	6	E36333	E36333 Analytical
10	41	100.0	720	6	AX004527	AX004527 Sequence
11	41	100.0	720	9	AF017256	AF017256 Homo sapi
12	41	100.0	738	11	BV177827	BV177827 sqnm97020
13	41	100.0	758	9	BC014098	BC014098 Homo sapi
14	41	100.0	177006	2	AC102691	AC102691 Mus muscu
15	41	100.0	255619	2	AC111772	AC111772 Rattus no
c 16	41	100.0	286562	2	AC137025	AC137025 Rattus no
17	41	100.0	309255	2	AC113219	AC113219 Rattus no
18	38	92.7	4887	10	AY383729	AY383729 Mus muscu
c 19	38	92.7	10029	1	AE010406	AE010406 Methanopy
c 20	38	92.7	69346	2	AC134394	AC134394 Homo sapi
21	38	92.7	133288	9	AL357503	AL357503 Human DNA
c 22	38	92.7	182003	9	AL355987	AL355987 Human DNA
23	38	92.7	187534	10	AC132251	AC132251 Mus muscu
c 24	38	92.7	210950	10	AC129317	AC129317 Mus muscu
c 25	38	92.7	212717	10	AL929228	AL929228 Mouse DNA
26	38	92.7	246070	2	AC135737	AC135737 Mus muscu
27	37	90.2	488	10	AY518351	AY518351 Rattus no
28	37	90.2	732	10	RNSDSYNGE	X86789 R.norvegicu
29	37	90.2	1275	6	CQ575643	CQ575643 Sequence
c 30	37	90.2	3275	6	CQ575642	CQ575642 Sequence
c 31	37	90.2	22723	2	AC019971	AC019971 Drosophil
32	37	90.2	89837	2	AC091822	AC091822 Homo sapi
c 33	37	90.2	90693	9	AC005592	AC005592 Homo sapi
c 34	37	90.2	96437	9	AY601819	AY601819 Homo sapi
c 35	37	90.2	110000	2	LMFLCHR36_10	Continuation (11 o
36	37	90.2	146000	9	AP005433	AP005433 Homo sapi
37	37	90.2	156870	2	AC149695	AC149695 Bos tauru
c 38	37	90.2	161117	3	AC008311	AC008311 Drosophil
39	37	90.2	162398	5	BX537341	BX537341 Zebrafish
c 40	37	90.2	168448	3	AC009346	AC009346 Drosophil
41	37	90.2	191734	2	AC016560	AC016560 Homo sapi
42	37	90.2	200146	2	AC073774	AC073774 Mus muscu
c 43	37	90.2	209523	10	AC084386	AC084386 Mus muscu
44	37	90.2	213050	1	AL646079	AL646079 Ralstonia
c 45	37	90.2	219405	2	AC118096	AC118096 Rattus no

ALIGNMENTS

RESULT 1
CR541790
LOCUS CR541790 381 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPDo834B0231D for gene SNCG, synuclein, gamma (breast cancer-specific protein 1); complete cds, without stopcodon.
ACCESSION CR541790
VERSION CR541790.1 GI:49456536
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 381)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 381)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

```
COMMENT     RZPD; RZPDo834B0231D, ORFNo 3631
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834B0231D RZPDLIB;
            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            Clone name at Harvard Institute of Proteomics
            (www.hip.harvard.edu): FLH130940.01L
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned without stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence BC014098
            we did not find any amino acid exchanges.
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES              Location/Qualifiers
     source           1. .381
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="RZPDo834B0231D"
                      /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                      /lab_host="DH5Alpha"
                      /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene             1. .381
                      /gene="SNCG"
     CDS              1. .>381
                      /gene="SNCG"
                      /codon_start=1
                      /protein_id="CAG46589.1"
                      /db_xref="GI:49456537"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              45.6          Length:         381
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     9             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x CR541790 (1-381)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        358 GAGGAGGCCCAGAGTGGGGGAGAC 381

RESULT 2
CR541788
LOCUS       CR541788                384 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens full open reading frame cDNA clone RZPDo834F0930D for
            gene SNCG, synuclein, gamma (breast cancer-specific protein 1);
            complete cds, incl. stopcodon.
ACCESSION   CR541788
VERSION     CR541788.1  GI:49456532
KEYWORDS    Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Cloning of human full open reading frames in Gateway(TM) system
            entry vector (pDONR201)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 384)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
            Germany
COMMENT     RZPD; RZPDo834F0930D, ORFNo 3605
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834F0930D RZPDLIB;
            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            Clone name at Harvard Institute of Proteomics
            (www.hip.harvard.edu): FLH131021.01X
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned incl. stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence BC014098
            we did not find any amino acid exchanges.
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES              Location/Qualifiers
     source           1. .384
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="RZPDo834F0930D"
                      /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                      /lab_host="DH5Alpha"
                      /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene             1. .384
                      /gene="SNCG"
     CDS              1. .384
                      /gene="SNCG"
                      /codon_start=1
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                      /db_xref="GI:49456533"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              45.9          Length:         384
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
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DB:                    9             Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x CR541788 (1-384)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        358 GAGGAGGCCCAGAGTGGGGGAGAC 381

RESULT 3
AF411524
LOCUS       AF411524                 488 bp    mRNA    linear   PRI 20-SEP-2001
DEFINITION  Homo sapiens synuclein gamma mRNA, complete cds.
ACCESSION   AF411524
VERSION     AF411524.1  GI:15705904
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Han,C., Zhang,B., Peng,X., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2001) Department of Biochemistry, Institute of
            Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong
            Dan San Tiao, Beijing 100005, P.R. China
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             12. .395
                     /note="SNCG; breast cancer-specific protein 1"
                     /codon_start=1
                     /product="synuclein gamma"
                     /protein_id="AAL05870.1"
                     /db_xref="GI:15705905"
                     /translation="MDVFKKGFSIAKEGVVDAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              56.4          Length:        488
Score:                  41.00         Matches:       8
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     9             Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x AF411524 (1-488)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 4
AR412236
LOCUS       AR412236                 550 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6639052.
ACCESSION   AR412236
VERSION     AR412236.1  GI:40167022
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Moore,P.A.
  TITLE     Human ADA2 polypeptides
  JOURNAL   Patent: US 6639052-A 1 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .550
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                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              62.5          Length:        550
Score:                  41.00         Matches:       8
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x AR412236 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 5
AX331171
LOCUS       AX331171                 550 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 1680 from Patent WO0194629.
ACCESSION   AX331171
VERSION     AX331171.1  GI:18121805
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 1680 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .550
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              62.5          Length:        550
Score:                  41.00         Matches:       8
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-09-017-715A-2_COPY_120_127 (1-8) x AX331171 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 6
BD022727
LOCUS       BD022727                 550 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Mammary cancer-specific gene 1.
ACCESSION   BD022727
VERSION     BD022727.1  GI:22563950
KEYWORDS    JP 2001509664-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Ji,H. and Rosen,C.A.
  TITLE     Mammary cancer-specific gene 1
  JOURNAL   Patent: JP 2001509664-A 1 24-JUL-2001;
            HUMAN GENOME SCIENCES INC
COMMENT     PN   JP 2001509664-A/1
            PD   24-JUL-2001
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            PF   03-FEB-1998 JP 1998515053
            PR   03-FEB-1997 US    60/037080
            PI   HONGJUN JI,CRAIG A ROSEN
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68,G01N33/574,C12N15/00,C12N5/00 CC
            Strandedness: Double;
            CC   Topology: Both;
            FH   Key             Location/Qualifiers
            FT   CDS             12. .392.
FEATURES              Location/Qualifiers
     source           1. .550
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                62.5          Length:         550
Score:                    41.00         Matches:        8
Percent Similarity:       100.00%       Conservative:   0
Best Local Similarity:    100.00%       Mismatches:     0
Query Match:              100.00%       Indels:         0
DB:                       6             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x BD022727 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 7
AF010126
LOCUS       AF010126                550 bp    mRNA    linear   PRI 26-JUL-1997
DEFINITION  Homo sapiens breast cancer-specific protein 1 (BCSG1) mRNA,
            complete cds.
ACCESSION   AF010126
VERSION     AF010126.1  GI:2281473
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K.,
            Rosen,C. and Shi,Y.E.
  TITLE     Identification of a breast cancer-specific gene, BCSG1, by direct
            differential cDNA sequencing
  JOURNAL   Cancer Res. 57 (4), 759-764 (1997)
  MEDLINE   97178957
   PUBMED   9044857
REFERENCE   2  (bases 1 to 550)
  AUTHORS   Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K.,
            Rosen,C. and Shi,Y.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUN-1997) Ped. Res., Long Island Jewish Medical
            Center, 270-05 76th Ave., New Hyde Park, NY 11040, USA
FEATURES              Location/Qualifiers
     source           1. .550
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="breast cancer"
                      /note="cDNA highly abundant in a breast cancer library but
                      not in normal library"
     gene             1. .550
                      /gene="BCSG1"
     CDS              12. .395
                      /gene="BCSG1"
                      /note="breast cancer-specific protein 1; synuclein-like;
                      AD amyloid-like"
                      /codon_start=1
                      /product="BCSG1 protein"
                      /protein_id="AAB64109.1"
                      /db_xref="GI:2281474"
                      /translation="MDVFKKGFSIAKKGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSKAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:                62.5          Length:         550
Score:                    41.00         Matches:        8
Percent Similarity:       100.00%       Conservative:   0
Best Local Similarity:    100.00%       Mismatches:     0
Query Match:              100.00%       Indels:         0
DB:                       9             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AF010126 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 8
CQ720882
LOCUS       CQ720882                704 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 6816 from Patent WO02068579.
ACCESSION   CQ720882
VERSION     CQ720882.1  GI:42281739
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 6816 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES              Location/Qualifiers
     source           1. .704
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                77.2          Length:         704
Score:                    41.00         Matches:        8
Percent Similarity:       100.00%       Conservative:   0
Best Local Similarity:    100.00%       Mismatches:     0
Query Match:              100.00%       Indels:         0
DB:                       6             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x CQ720882 (1-704)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        405 GAGGAGGCCCAGAGTGGGGGAGAC 428

RESULT 9
E36333
LOCUS       E36333                  720 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Analytical matter based on synuclein and novel synuclein protein.
ACCESSION   E36333
VERSION     E36333.1  GI:13022626
KEYWORDS    JP 1999239488-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
```

```
  AUTHORS   Andrew,S.M., Valdimia,R.B. and Arun,M.D.
  TITLE     Analytical matter based on synuclein and novel synuclein protein
  JOURNAL   Patent: JP 1999239488-A 1 07-SEP-1999;
            THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS,NYUROBA LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 1999239488-A/1
            PD   07-SEP-1999
            PF   21-SEP-1998 JP 1998306283
            PR   19-SEP-1997 GB    9719879.0
            PI   ANDREW SMITH MAKKARION,VALDIMIA RUVOVICHI BUCHIMAN, PI   ARUN
            MILWARD DAVIS
            PC   C12N15/09,A01K67/027,C12Q1/68,G01N33/53,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   CDS             (49). .(432).
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              78.7          Length:         720
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     6             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x E36333 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 10
AX004527
LOCUS       AX004527                720 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 1 from Patent EP0908727.
ACCESSION   AX004527
VERSION     AX004527.1  GI:9927977
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   .
  TITLE     Synuclein-based assay and synuclein protein
  JOURNAL   Patent: EP 0908727-A 1 14-APR-1999;
            NEUROPA LIMITED (GB); UNIV COURT OF THE UNIVERSITY O (GB)
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
     CDS              49. .432
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAC04899.1"
                      /db_xref="GI:9927978"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGVASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              78.7          Length:         720
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     6             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AX004527 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 11
AF017256
LOCUS       AF017256                720 bp    mRNA    linear   PRI 23-SEP-1998
DEFINITION  Homo sapiens persyn mRNA, complete cds.
ACCESSION   AF017256
VERSION     AF017256.1  GI:3642774
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ninkina,N.N., Alimova-Kost,M.V., Paterson,J.W., Delaney,L.,
            Cohen,B.B., Imreh,S., Gnuchev,N.V., Davies,A.M. and Buchman,V.L.
  TITLE     Organization, expression and polymorphism of the human persyn gene
  JOURNAL   Hum. Mol. Genet. 7 (9), 1417-1424 (1998)
  MEDLINE   98367030
   PUBMED   9700196
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Buchman,V.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-1997) School of Biomedical Sciences, Univ. of St.
            Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
            Scotland
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
     5'UTR            1. .48
     CDS              49. .432
                      /note="member of the synuclein family with a distinct
                      pattern of expression"
                      /codon_start=1
                      /product="persyn"
                      /protein_id="AAC36550.1"
                      /db_xref="GI:3642775"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGVASKEKEEVAEEAQSGGD"
     3'UTR            433. .720
     polyA_signal     684. .689
     polyA_site       706
ORIGIN

Alignment Scores:
Pred. No.:              78.7          Length:         720
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     9             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AF017256 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 12
BV177827
LOCUS       BV177827                738 bp    DNA     linear   STS 10-JUN-2004
DEFINITION  sqnm97020 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
            tagged site.
ACCESSION   BV177827
VERSION     BV177827.1  GI:48014020
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KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 738)
AUTHORS Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
JOURNAL Genome Res. (2004) In press
COMMENT
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 738.

FEATURES	Location/Qualifiers
source	1. .738
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/clone_lib="Human DNA (Sequenom)"
STS	<1. .>738

ORIGIN

Alignment Scores:

Pred. No.:	80.4	Length:	738
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x BV177827 (1-738)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        408 GAGGAGGCCCAGAGTGGGGGAGAC 431
```

RESULT 13
BC014098
LOCUS BC014098 758 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens synuclein, gamma (breast cancer-specific protein 1), mRNA (cDNA clone MGC:20132 IMAGE:4546444), complete cds.
ACCESSION BC014098
VERSION BC014098.2 GI:33878363
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 758)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 758)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT On Aug 19, 2003 this sequence version replaced gi:15559464.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 28 Row: p Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507112.

FEATURES	Location/Qualifiers
source	1. .758
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="MGC:20132 IMAGE:4546444"
	/tissue_type="Colon, adenocarcinoma"
	/clone_lib="NIH_MGC_15"
	/lab_host="DH10B-R"
	/note="Vector: pOTB7"
gene	1. .758
	/gene="SNCG"
	/note="synonyms: SR, BCSG1"
	/db_xref="LocusID:6623"
	/db_xref="MIM:602998"
CDS	71. .454
	/gene="SNCG"
	/codon_start=1
	/product="synuclein, gamma (breast cancer-specific protein 1)"
	/protein_id="AAH14098.1"
	/db_xref="GI:15559465"
	/db_xref="LocusID:6623"
	/db_xref="MIM:602998"
	/translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP SAPQQEGEASKEKEEVAEEAQSGGD"

ORIGIN

Alignment Scores:

Pred. No.:	82.2	Length:	758
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0

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Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     9             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x BC014098 (1-758)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        428 GAGGAGGCCCAGAGTGGGGGAGAC 451

RESULT 14
AC102691
LOCUS       AC102691               177006 bp    DNA     linear   HTG 31-MAR-2004
DEFINITION  Mus musculus chromosome 10 clone RP24-273A2 map 10, *** SEQUENCING
            IN PROGRESS ***, 6 unordered pieces.
ACCESSION   AC102691
VERSION     AC102691.3  GI:45861072
KEYWORDS    HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 177006)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 10, clone RP24-273A2
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 177006)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 177006)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
            DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
            Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
            Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
            Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
            MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
            Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
            Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 31, 2004 this sequence version replaced gi:22325140.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@broad.mit.edu
            -------------- Project Information
                Center project name: L19270
                Center clone name: 273_A_2
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    88876: contig of 88876 bp in length
            *   88877    88976: gap of 100 bp
            *   88977    96251: contig of 7275 bp in length
            *   96252    96351: gap of 100 bp
            *   96352   119842: contig of 23491 bp in length
            *  119843   119942: gap of 100 bp
            *  119943   131510: contig of 11568 bp in length
            *  131511   131610: gap of 100 bp
            *  131611   145791: contig of 14181 bp in length
            *  145792   145891: gap of 100 bp
            *  145892   177006: contig of 31115 bp in length.
FEATURES             Location/Qualifiers
     source          1. .177006
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="10"
                     /map="10"
                     /clone="RP24-273A2"
                     /clone_lib="RPCI-24 Male Mouse BAC"
ORIGIN

Alignment Scores:
Pred. No.:              8.84e+03        Length:         177006
Score:                  41.00           Matches:        8
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AC102691 (1-177006)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db      32827 GAAGAAGCCCAGAGCGGTGGAGAC 32850

RESULT 15
AC111772
LOCUS       AC111772               255619 bp    DNA     linear   HTG 15-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-169C7, *** SEQUENCING IN PROGRESS
            ***, 6 unordered pieces.
ACCESSION   AC111772
VERSION     AC111772.4  GI:25007013
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
```

```
          Rattus.
REFERENCE 1  (bases 1 to 255619)
  AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
          Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
          Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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          Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
          Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
          Weinstock,G. and Gibbs,R.A.
  TITLE   Direct Submission
  JOURNAL Unpublished
REFERENCE 2  (bases 1 to 255619)
  AUTHORS Worley,K.C.
  TITLE   Direct Submission
  JOURNAL Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
          of Molecular and Human Genetics, Baylor College of Medicine, One
          Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3  (bases 1 to 255619)
  AUTHORS Rat Genome Sequencing Consortium.
  TITLE   Direct Submission
  JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
          of Molecular and Human Genetics, Baylor College of Medicine, One
          Baylor Plaza, Houston, TX 77030, USA
COMMENT   On Nov 15, 2002 this sequence version replaced gi:23665002.
          The sequence in this assembly is a combination of BAC based reads
          and whole genome shotgun sequencing reads assembled using Atlas
          (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
          in the feature table below represents a scaffold in the Atlas
          assembly (a 'contig-scaffold'). Within each contig-scaffold,
          individual sequence contigs are ordered and oriented, and separated
          by sized gaps filled with Ns to the estimated size. The sequence
          may extend beyond the ends of the clone and there may be sequence
          contigs within a contig-scaffold that consist entirely of whole
          genome shotgun sequence reads. Both end sequences and whole genome
          shotgun sequence only contigs will be indicated in the feature
          table.
          -------------- Genome Center
              Center: Baylor College of Medicine
              Center code: BCM
              Web site: http://www.hgsc.bcm.tmc.edu/
              Contact: hgsc-help@bcm.tmc.edu
          -------------- Project Information
              Center project name: GOBO
              Center clone name: CH230-169C7
          -------------- Summary Statistics
              Assembly program: Phrap; version 0.990329
              Consensus quality: 212404 bases at least Q40
              Consensus quality: 215959 bases at least Q30
              Consensus quality: 217955 bases at least Q20
              Estimated insert size: 218715; sum-of-contigs estimation
              Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
          --------------
          * NOTE: Estimated insert size may differ from sequence length
          *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 6 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *        1     7834: contig of 7834 bp in length
          *     7835     7934: gap of unknown length
          *     7935    18981: contig of 11047 bp in length
          *    18982    19081: gap of unknown length
          *    19082    62574: contig of 43493 bp in length
          *    62575    62674: gap of unknown length
          *    62675    65974: contig of 3300 bp in length
          *    65975    66074: gap of unknown length
          *    66075   254373: contig of 188299 bp in length
          *   254374   254473: gap of unknown length
          *   254474   255619: contig of 1146 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     /clone="CH230-169C7"
     misc_feature    complement(6736. .7529)
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                     clone_end:Sp6
                     site:
                     end_sequence:BH336366"
     misc_feature    7935. .9481
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ORIGIN

Alignment Scores:
Pred. No.:              1.21e+04        Length:         255619
Score:                  41.00           Matches:        8
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AC111772 (1-255619)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
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Db 223025 GAAGAAGCACAGAGTGGAGGGGAC 223048

Search completed: May 4, 2005, 11:54:02
Job time : 489.669 secs

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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:55 ; Search time 7212.58 Seconds
(without alignments)
853.206 Million cell updates/sec

Title: US-09-017-715A-2
Perfect score: 610
Sequence: 1 MDVFKKGFSIAKKGVVGAVE.....EGEASKEKEEVAEEAQSGGD 127

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	610	100.0	550	6	AR412236	AR412236 Sequence
2	610	100.0	550	6	AX331171	AX331171 Sequence
3	610	100.0	550	6	BD022727	BD022727 Mammary c
4	610	100.0	550	9	AF010126	AF010126 Homo sapi
5	602	98.7	381	9	CR541790	CR541790 Homo sapi
6	602	98.7	384	9	CR541788	CR541788 Homo sapi
7	602	98.7	704	6	CQ720882	CQ720882 Sequence
8	602	98.7	758	9	BC014098	BC014098 Homo sapi
9	595	97.5	488	9	AF411524	AF411524 Homo sapi
10	595	97.5	720	6	E36333	E36333 Analytical
11	595	97.5	720	6	AX004527	AX004527 Sequence
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13	532.5	87.3	738	11	BV177827	BV177827 sqnm97020
14	523	85.7	677	4	AF219257	AF219257 Bos tauru
15	497	81.5	727	6	E36334	E36334 Analytical
16	497	81.5	727	6	AX004529	AX004529 Sequence
17	497	81.5	727	10	AF017255	AF017255 Mus muscu
18	497	81.5	748	10	BC028508	BC028508 Mus muscu
19	476	78.0	488	10	AY518351	AY518351 Rattus no
20	470	77.0	732	10	RNSDSYNGE	X86789 R.norvegicu
21	438.5	71.9	873	5	AF253513	AF253513 Gallus ga
22	412	67.5	1120	5	CR762140	CR762140 Xenopus t
23	399.5	65.5	1046	5	BC054269	BC054269 Xenopus l
24	398.5	65.3	1040	5	AY055119	AY055119 Xenopus l
25	388.5	63.7	1180	5	BC072217	BC072217 Xenopus l
26	316	51.8	695	10	S73007	S73007 synuclein S
27	316	51.8	1017	10	AY550005	AY550005 Rattus no
28	316	51.8	1017	10	AY550006	AY550006 Rattus no
29	316	51.8	1018	10	AF007758	AF007758 Rattus no
30	316	51.8	1047	10	BC046764	BC046764 Mus muscu
31	316	51.8	1124	10	AF033261	AF033261 Mus muscu
32	316	51.8	1181	10	AF179273	AF179273 Mus muscu
33	315	51.6	695	10	S73008	S73008 synuclein S
34	314.5	51.6	1234	5	SEISYNELFI	L33860 Serinus can
35	311.5	51.1	1182	5	AF253512	AF253512 Gallus ga
36	311.5	51.1	1190	5	BX936116	BX936116 Gallus ga
37	311	51.0	1233	5	BC054200	BC054200 Xenopus l
38	310	50.8	513	10	AF044672	AF044672 Mus muscu
39	308	50.5	549	10	RAT14KDAP	D17764 Rattus sp.
40	307.5	50.4	420	9	CR541653	CR541653 Homo sapi
41	307.5	50.4	423	6	AX662310	AX662310 Sequence
42	307.5	50.4	423	9	CR457058	CR457058 Homo sapi
43	307.5	50.4	423	12	BT007765	BT007765 Synthetic
44	307.5	50.4	425	9	AY049786	AY049786 Homo sapi
45	307.5	50.4	546	6	CQ728889	CQ728889 Sequence

ALIGNMENTS

RESULT 1
AR412236
LOCUS AR412236 550 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6639052.
ACCESSION AR412236
VERSION AR412236.1 GI:40167022
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 550)
AUTHORS Moore,P.A.
TITLE Human ADA2 polypeptides
JOURNAL Patent: US 6639052-A 1 28-OCT-2003;
FEATURES Location/Qualifiers
source 1. .550
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 7.25e-44 Length: 550
Score: 610.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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US-09-017-715A-2 (1-127) x AR412236 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
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Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 2
AX331171
LOCUS       AX331171                 550 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 1680 from Patent WO0194629.
ACCESSION   AX331171
VERSION     AX331171.1  GI:18121805
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 1680 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .550
                     /organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.:              7.25e-44        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-017-715A-2 (1-127) x AX331171 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 3
BD022727
LOCUS       BD022727                 550 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Mammary cancer-specific gene 1.
ACCESSION   BD022727
VERSION     BD022727.1  GI:22563950
KEYWORDS    JP 2001509664-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Ji,H. and Rosen,C.A.
  TITLE     Mammary cancer-specific gene 1
  JOURNAL   Patent: JP 2001509664-A 1 24-JUL-2001;
            HUMAN GENOME SCIENCES INC
COMMENT     PN   JP 2001509664-A/1
            PD   24-JUL-2001
            PF   03-FEB-1998 JP 1998515053
            PR   03-FEB-1997 US    60/037080
            PI   HONGJUN JI,CRAIG A ROSEN
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68,G01N33/574,C12N15/00,C12N5/00 CC
            Strandedness: Double;
            CC   Topology: Both;
            FH   Key             Location/Qualifiers
            FT   CDS             12. .392.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              7.25e-44        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-017-715A-2 (1-127) x BD022727 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131
```

```
Qy          41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy          61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy          81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy         101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy         121 GluAlaGlnSerGlyGlyAsp 127
               |||||||||||||||||||
Db         372 GAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 4
AF010126
LOCUS AF010126 550 bp mRNA linear PRI 26-JUL-1997
DEFINITION Homo sapiens breast cancer-specific protein 1 (BCSG1) mRNA, complete cds.
ACCESSION AF010126
VERSION AF010126.1 GI:2281473 Feb 15th
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K., Rosen,C. and Shi,Y.E.
TITLE Identification of a breast cancer-specific gene, BCSG1, by direct differential cDNA sequencing
JOURNAL Cancer Res. 57 (4), 759-764 (1997)
MEDLINE 97178957
PUBMED 9044857
REFERENCE 2 (bases 1 to 550)
AUTHORS Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K., Rosen,C. and Shi,Y.E.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-1997) Ped. Res., Long Island Jewish Medical Center, 270-05 76th Ave., New Hyde Park, NY 11040, USA
FEATURES Location/Qualifiers
source 1. .550
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="breast cancer"
/note="cDNA highly abundant in a breast cancer library but not in normal library"
gene 1. .550
/gene="BCSG1"
CDS 12. .395
/gene="BCSG1"
/note="breast cancer-specific protein 1; synuclein-like; AD amyloid-like"
/codon_start=1
/product="BCSG1 protein"
/protein_id="AAB64109.1"
/db_xref="GI:2281474"
/translation="MDVFKKGFSIAKKGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKTKENVVQSVTSVAEKTKEQANAVSKAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRPSAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.: 7.25e-44 Length: 550
Score: 610.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-017-715A-2 (1-127) x AF010126 (1-550)

```
Qy           1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Db          12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy          21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy          41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy          61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy          81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy         101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy         121 GluAlaGlnSerGlyGlyAsp 127
               |||||||||||||||||||
Db         372 GAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 5
CR541790
LOCUS CR541790 381 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPDo834B0231D for gene SNCG, synuclein, gamma (breast cancer-specific protein 1); complete cds, without stopcodon.
ACCESSION CR541790
VERSION CR541790.1 GI:49456536
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 381)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 381)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
COMMENT RZPD; RZPDo834B0231D, ORFNo 3631
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834B0231D RZPDLIB; Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100

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          Fax: +49 30 32639 111
          www.rzpd.de
          This clone is available from RZPD;
          Contact RZPD (customer.service@rzpd.de) for further information.
          Clone name at Harvard Institute of Proteomics
          (www.hip.harvard.edu): FLH130940.01L
          This CDS clone is part of a collection of human full ORF clones
          jointly established and verified by the Harvard Institute of
          Proteomics (HIP) and RZPD.
          This CDS has been cloned without stopcodon.
          The CDS has been inserted into pDONR201 via a BP Clonase(TM)
          reaction. Additional sequence has been added in front of the start
          codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
          The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att
          The clone is validated by full sequence check.
          Compared to the reference sequence BC014098
          we did not find any amino acid exchanges.
          Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES             Location/Qualifiers
     source          1. .381
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="RZPDo834B0231D"
                     /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                     /lab_host="DH5Alpha"
                     /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene            1. .381
                     /gene="SNCG"
     CDS             1. .>381
                     /gene="SNCG"
                     /codon_start=1
                     /protein_id="CAG46589.1"
                     /db_xref="GI:49456537"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              2.38e-43        Length:         381
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2 (1-127) x CR541790 (1-381)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db          1 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 60

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 120

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 180

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 240

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 300

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 360

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        361 GAGGCCCAGAGTGGGGGAGAC 381

RESULT 6
CR541788
LOCUS       CR541788                384 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens full open reading frame cDNA clone RZPDo834F0930D for
            gene SNCG, synuclein, gamma (breast cancer-specific protein 1);
            complete cds, incl. stopcodon.
ACCESSION   CR541788
VERSION     CR541788.1  GI:49456532
KEYWORDS    Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Cloning of human full open reading frames in Gateway(TM) system
            entry vector (pDONR201)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 384)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
            Germany
COMMENT     RZPD; RZPDo834F0930D, ORFNo 3605
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834F0930D RZPDLIB;
            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            Clone name at Harvard Institute of Proteomics
            (www.hip.harvard.edu): FLH131021.01X
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned incl. stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence BC014098
            we did not find any amino acid exchanges.
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="RZPDo834F0930D"
                     /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                     /lab_host="DH5Alpha"
                     /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene            1. .384
                     /gene="SNCG"
     CDS             1. .384
                     /gene="SNCG"
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                     /codon_start=1
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                     /db_xref="GI:49456533"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              2.4e-43       Length:         384
Score:                  602.00        Matches:        125
Percent Similarity:     100.00%       Conservative:   2
Best Local Similarity:  98.43%        Mismatches:     0
Query Match:            98.69%        Indels:         0
DB:                     9             Gaps:           0

US-09-017-715A-2 (1-127) x CR541788 (1-384)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db          1 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 60

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Db         61 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 120

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        121 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 180

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 240

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 300

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 360

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||||
Db        361 GAGGCCCAGAGTGGGGGAGAC 381

RESULT 7
CQ720882
LOCUS       CQ720882                704 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 6816 from Patent WO02068579.
ACCESSION   CQ720882
VERSION     CQ720882.1  GI:42281739
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 6816 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .704
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              4.59e-43      Length:         704
Score:                  602.00        Matches:        125
Percent Similarity:     100.00%       Conservative:   2
Best Local Similarity:  98.43%        Mismatches:     0
Query Match:            98.69%        Indels:         0
DB:                     6             Gaps:           0

US-09-017-715A-2 (1-127) x CQ720882 (1-704)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         48 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 107

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 167

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 227

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Db        228 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 287

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 347

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 407

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||||
Db        408 GAGGCCCAGAGTGGGGGAGAC 428

RESULT 8
BC014098
LOCUS       BC014098                758 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens synuclein, gamma (breast cancer-specific protein 1),
            mRNA (cDNA clone MGC:20132 IMAGE:4546444), complete cds.
ACCESSION   BC014098
VERSION     BC014098.2  GI:33878363
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 758)
  AUTHORS   Strausberg,R.
```

```
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 19, 2003 this sequence version replaced gi:15559464.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 28 Row: p Column: 20
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4507112.
FEATURES             Location/Qualifiers
     source          1. .758
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:20132 IMAGE:4546444"
                     /tissue_type="Colon, adenocarcinoma"
                     /clone_lib="NIH_MGC_15"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene            1. .758
                     /gene="SNCG"
                     /note="synonyms: SR, BCSG1"
                     /db_xref="LocusID:6623"
                     /db_xref="MIM:602998"
     CDS             71. .454
                     /gene="SNCG"
                     /codon_start=1
                     /product="synuclein, gamma (breast cancer-specific protein
                     1)"
                     /protein_id="AAH14098.1"
                     /db_xref="GI:15559465"
                     /db_xref="LocusID:6623"
                     /db_xref="MIM:602998"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              4.97e-43        Length:         758
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2 (1-127) x BC014098 (1-758)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Db         71 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 130

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 190

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 250

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        251 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 310

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 370

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 430

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        431 GAGGCCCAGAGTGGGGGAGAC 451

RESULT 9
AF411524
LOCUS       AF411524                 488 bp    mRNA    linear   PRI 20-SEP-2001
DEFINITION  Homo sapiens synuclein gamma mRNA, complete cds.
ACCESSION   AF411524
VERSION     AF411524.1  GI:15705904
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Han,C., Zhang,B., Peng,X., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2001) Department of Biochemistry, Institute of
            Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong
            Dan San Tiao, Beijing 100005, P.R. China
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             12. .395
                     /note="SNCG; breast cancer-specific protein 1"
                     /codon_start=1
                     /product="synuclein gamma"
                     /protein_id="AAL05870.1"
                     /db_xref="GI:15705905"
                     /translation="MDVFKKGFSIAKEGVVDAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGEASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:              1.24e-42        Length:         488
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2 (1-127) x AF411524 (1-488)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Db         12 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGATGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
                 ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
                 |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 10
E36333
LOCUS       E36333                  720 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Analytical matter based on synuclein and novel synuclein protein.
ACCESSION   E36333
VERSION     E36333.1  GI:13022626
KEYWORDS    JP 1999239488-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Andrew,S.M., Valdimia,R.B. and Arun,M.D.
  TITLE     Analytical matter based on synuclein and novel synuclein protein
  JOURNAL   Patent: JP 1999239488-A 1 07-SEP-1999;
            THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS,NYUROBA LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 1999239488-A/1
            PD   07-SEP-1999
            PF   21-SEP-1998 JP 1998306283
            PR   19-SEP-1997 GB    9719879.0
            PI   ANDREW SMITH MAKKARION,VALDIMIA RUVOVICHI BUCHIMAN, PI   ARUN
            MILWARD DAVIS
            PC   C12N15/09,A01K67/027,C12Q1/68,G01N33/53,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   CDS             (49). .(432).
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
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                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.88e-42        Length:         720
Score:                    595.00          Matches:        124
Percent Similarity:       99.21%          Conservative:   2
Best Local Similarity:    97.64%          Mismatches:     1
Query Match:              97.54%          Indels:         0
DB:                       6               Gaps:           0

US-09-017-715A-2 (1-127) x E36333 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Db         49 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
                 ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                 ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
                 |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 11
AX004527
LOCUS       AX004527                720 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 1 from Patent EP0908727.
ACCESSION   AX004527
VERSION     AX004527.1  GI:9927977
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   .
  TITLE     Synuclein-based assay and synuclein protein
  JOURNAL   Patent: EP 0908727-A 1 14-APR-1999;
            NEUROPA LIMITED (GB); UNIV COURT OF THE UNIVERSITY O (GB)
FEATURES              Location/Qualifiers
     source           1. .720
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
     CDS              49. .432
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAC04899.1"
                      /db_xref="GI:9927978"
                      /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                      KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                      SAPQQEGVASKEKEEVAEEAQSGGD"
ORIGIN

Alignment Scores:
Pred. No.:                1.88e-42        Length:         720
Score:                    595.00          Matches:        124
Percent Similarity:       99.21%          Conservative:   2
Best Local Similarity:    97.64%          Mismatches:     1
Query Match:              97.54%          Indels:         0
DB:                       6               Gaps:           0

US-09-017-715A-2 (1-127) x AX004527 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
                 ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         49 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228
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Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 12
AF017256
LOCUS       AF017256               720 bp    mRNA    linear   PRI 23-SEP-1998
DEFINITION  Homo sapiens persyn mRNA, complete cds.
ACCESSION   AF017256
VERSION     AF017256.1  GI:3642774
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ninkina,N.N., Alimova-Kost,M.V., Paterson,J.W., Delaney,L.,
            Cohen,B.B., Imreh,S., Gnuchev,N.V., Davies,A.M. and Buchman,V.L.
  TITLE     Organization, expression and polymorphism of the human persyn gene
  JOURNAL   Hum. Mol. Genet. 7 (9), 1417-1424 (1998)
  MEDLINE   98367030
   PUBMED   9700196
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Buchman,V.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-1997) School of Biomedical Sciences, Univ. of St.
            Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
            Scotland
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     5'UTR           1. .48
     CDS             49. .432
                     /note="member of the synuclein family with a distinct
                     pattern of expression"
                     /codon_start=1
                     /product="persyn"
                     /protein_id="AAC36550.1"
                     /db_xref="GI:3642775"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
                     KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                     SAPQQEGVASKEKEEVAEEAQSGGD"
     3'UTR           433. .720
     polyA_signal    684. .689
     polyA_site      706
ORIGIN

Alignment Scores:
Pred. No.:              1.88e-42        Length:         720
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2 (1-127) x AF017256 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Db         49 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 13
BV177827
LOCUS       BV177827               738 bp    DNA     linear   STS 10-JUN-2004
DEFINITION  sqnm97020 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
            tagged site.
ACCESSION   BV177827
VERSION     BV177827.1  GI:48014020
KEYWORDS    STS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 738)
  AUTHORS   Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
            Cantor,C.R. and Braun,A.
  TITLE     Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
            Regions
  JOURNAL   Genome Res. (2004) In press
COMMENT
            Contact: Andreas Braun
            Pharmaceuticals division
            Sequenom, Inc.
            3595 John Hopkins Court, San Diego, CA 92121, USA
            Tel: 18582029018
            Fax: 18582029020
            Email: abraun@sequenom.com
            Primer A: No primer sequence submitted
            Primer B: No primer sequence submitted
            STS size: 738.
FEATURES             Location/Qualifiers
     source          1. .738
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Human DNA (Sequenom)"
     STS             <1. .>738
ORIGIN

Alignment Scores:
Pred. No.:              4.48e-37        Length:         738
Score:                  532.50          Matches:        120
Percent Similarity:     96.06%          Conservative:   2
Best Local Similarity:  94.49%          Mismatches:     5
Query Match:            87.30%          Indels:         2
DB:                     11              Gaps:           0
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US-09-017-715A-2 (1-127) x BV177827 (1-738)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         53 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 112

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
                 |||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db        113 TAGACCAAGCAGTGTGTTACGGAAGCAGCTGAGAAGACCAAGGAGGGGTC-ATGTATGT- 170

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 230

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Db        231 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 290

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 350

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        351 AGGCCATCTGCCCCCCAACAGGAGGGTGWGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 410

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        411 GAGGCCCAGAGTGGGGGAGAC 431

RESULT 14
AF219257
LOCUS       AF219257                677 bp    mRNA    linear   MAM 09-FEB-2000
DEFINITION  Bos taurus synoretin mRNA, complete cds.
ACCESSION   AF219257
VERSION     AF219257.1  GI:6942173
KEYWORDS    .
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Surguchov,A., Surgucheva,I., Solessio,E. and Baehr,W.
  TITLE     Synoretin--A new protein belonging to the synuclein family
  JOURNAL   Mol. Cell. Neurosci. 13 (2), 95-103 (1999)
  MEDLINE   99210388
   PUBMED   10192768
REFERENCE   2  (bases 1 to 677)
  AUTHORS   Surguchov,A., Surgucheva,I., Baehr,W. and Solessio,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-DEC-1999) Ophthalmology, Washington University School
            of Medicine in St. Louis, 660 South Euclid, St. Louis, MO 63108,
            USA
FEATURES             Location/Qualifiers
     source          1. .677
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
     CDS             1. .384
                     /note="member of gamma-subfamily of synuclein; similar to
                     persyn; expressed in retina and brain"
                     /codon_start=1
                     /product="synoretin"
                     /protein_id="AAF32342.1"
                     /db_xref="GI:6942174"
                     /translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
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ORIGIN

Alignment Scores:
Pred. No.:              2.67e-36        Length:         677
Score:                  523.00          Matches:        109
Percent Similarity:     91.34%          Conservative:   7
Best Local Similarity:  85.83%          Mismatches:     11
Query Match:            85.74%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2 (1-127) x AF219257 (1-677)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db          1 ATGGACGTCTTCAAGAAGGGTTTCTCCATTGCCAAGGAGGGTGTGGTGGGTGCCGTGGAA 60

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGACCAAACAGGGAGTGACAGAGGCAGCTGAGAAGACCAAGGAGGGTGTCATGTATGTG 120

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        121 GGAGCTAAGACCAAAGAGGGTGTTGTGCAGAGTGTGACTTCAGTGGCTGAGAAGACCAAG 180

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGGCCAACGCCGTGAGTGAGGCCGTGGTCTCCAGTGTCAACACTGTGGCCACCAAG 240

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||   ||||||||||||||||||||||||||||||   ||||||   |||
Db        241 ACTGTGGAGGAGGTGGAGAACATTGCAGTCACCTCTGGAGTGGTGCACAAGGAGGCCCTG 300

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              :::         |||   ||||||   ||||||:::|||   :::|||:::||||||||||
Db        301 AAGCAACCTGTCCCCTCACAGGAGGATGAGGCAGCCAAAGCGGAAGAGCAAGTGGCTGAG 360

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||   :::|||||||||||||
Db        361 GAGACCAAGAGTGGGGGAGAT 381

RESULT 15
E36334
LOCUS       E36334                  727 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Analytical matter based on synuclein and novel synuclein protein.
ACCESSION   E36334
VERSION     E36334.1  GI:13022627
KEYWORDS    JP 1999239488-A/2.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 727)
  AUTHORS   Andrew,S.M., Valdimia,R.B. and Arun,M.D.
  TITLE     Analytical matter based on synuclein and novel synuclein protein
  JOURNAL   Patent: JP 1999239488-A 2 07-SEP-1999;
            THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS,NYUROBA LTD
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1999239488-A/2
            PD   07-SEP-1999
            PF   21-SEP-1998 JP 1998306283
            PR   19-SEP-1997 GB    9719879.0
            PI   ANDREW SMITH MAKKARION,VALDIMIA RUVOVICHI BUCHIMAN, PI   ARUN
            MILWARD DAVIS
            PC   C12N15/09,A01K67/027,C12Q1/68,G01N33/53,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   CDS             (69). .(440).
FEATURES             Location/Qualifiers
     source          1. .727
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
ORIGIN

Alignment Scores:
Pred. No.:              4.93e-34        Length:         727
Score:                  497.00          Matches:        108
Percent Similarity:     89.76%          Conservative:   6
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Best Local Similarity: 85.04% Mismatches: 9
Query Match: 81.48% Indels: 4
DB: 6 Gaps: 2

US-09-017-715A-2 (1-127) x E36334 (1-727)

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Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         69 ATGGACGTCTTCAAGAAAGGCTTCTCCATTGCCAAGGAAGGTGTTGTGGGTGCTGTAGAA 128

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 AAGACCAAGCAGGGAGTAACGGAGGCAGCTGAGAAGACCAAGGAGGGGGTTATGTATGTG 188

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GGCACCAAAACCAAGGAGAACGTGGTACAAAGTGTCACCTCAGTGGCTGAGAAGACCAAG 248

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||   |||
Db        249 GAGCAGGCCAATGCCGTGAGTGAAGCTGTGGTCAGCAGCGTCAACACAGTGGCCAACAAG 308

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||   ||||||:::||||||||||||||||||||||||||
Db        309 ACCGTGGAGGAGGCTGAAAACATCGTGGTCACCACCGGGGTGGTGCGCAAGGAGGACTTG 368

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                 |||   |||      ||||||         :::||||||:::||||||      |||
Db        369 GAACCCCCTGCACAGGACCAAGAA---------GCCAAAGAGCAAGAGGAG---AATGAA 416

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              ||||||:::||||||   |||
Db        417 GAGGCCAAGAGTGGAGAAGAC 437
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Search completed: May 4, 2005, 11:53:21
Job time : 7221.91 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 10:17:21 ; Search time 65.0738 Seconds
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Title: US-09-017-715A-2_COPY_120_127
Perfect score: 41
Sequence: 1 EEAQSGGD 8

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		41	100.0	384	19	US-10-826-157-5	Sequence 5, Appli
2		41	100.0	478	9	US-09-925-298-172	Sequence 172, App
3		41	100.0	478	14	US-10-102-806-172	Sequence 172, App
4		41	100.0	479	10	US-09-918-995-2705	Sequence 2705, Ap
5		41	100.0	550	9	US-09-954-531-613	Sequence 613, App
6		41	100.0	550	17	US-10-453-478-1	Sequence 1, Appli
7		41	100.0	550	19	US-10-843-641A-1680	Sequence 1680, Ap
8		41	100.0	720	14	US-10-097-340-297	Sequence 297, App
9		41	100.0	720	17	US-10-282-174-469	Sequence 469, App
10		41	100.0	720	19	US-10-600-009-469	Sequence 469, App
11		41	100.0	796	9	US-09-925-298-171	Sequence 171, App
12		41	100.0	796	14	US-10-102-806-171	Sequence 171, App
13	c	38	92.7	1125	17	US-10-369-493-33286	Sequence 33286, A
14	c	37	90.2	442	18	US-10-425-115-90466	Sequence 90466, A
15		37	90.2	2185	18	US-10-437-963-8217	Sequence 8217, Ap
16	c	37	90.2	106236	19	US-10-741-600-17759	Sequence 17759, A
17	c	36	87.8	357	18	US-10-437-963-43087	Sequence 43087, A
18		36	87.8	406	17	US-10-424-599-15323	Sequence 15323, A
19		36	87.8	1174	13	US-10-027-632-123222	Sequence 123222,
20		36	87.8	1174	13	US-10-027-632-123223	Sequence 123223,
21		36	87.8	1174	17	US-10-027-632-123222	Sequence 123222,
22		36	87.8	1174	17	US-10-027-632-123223	Sequence 123223,
23		36	87.8	2116	17	US-10-104-047-1099	Sequence 1099, Ap
24		36	87.8	3016	18	US-10-602-494-48	Sequence 48, Appl
25	c	36	87.8	4985	13	US-10-071-223-1	Sequence 1, Appli
26	c	36	87.8	4985	19	US-10-896-552-1	Sequence 1, Appli
27		36	87.8	5372	18	US-10-723-860-8187	Sequence 8187, Ap
28	c	36	87.8	5515	9	US-09-751-100B-98	Sequence 98, Appl
29	c	36	87.8	2256646	18	US-10-470-565-1	Sequence 1, Appli
30	c	35	85.4	291	18	US-10-425-115-65435	Sequence 65435, A
31		35	85.4	397	18	US-10-767-701-27423	Sequence 27423, A
32		35	85.4	518	18	US-10-021-323-3503	Sequence 3503, Ap
33	c	35	85.4	547	16	US-10-029-386-6547	Sequence 6547, Ap
34	c	35	85.4	588	18	US-10-437-963-6679	Sequence 6679, Ap
35	c	35	85.4	775	17	US-10-425-114-6521	Sequence 6521, Ap
36	c	35	85.4	775	18	US-10-425-115-10074	Sequence 10074, A
37	c	35	85.4	884	18	US-10-425-115-119416	Sequence 119416,
38	c	35	85.4	918	17	US-10-369-493-44914	Sequence 44914, A
39	c	35	85.4	1273	14	US-10-198-846-12657	Sequence 12657, A
40	c	35	85.4	1672	18	US-10-425-115-145170	Sequence 145170,
41	c	35	85.4	1836	17	US-10-424-599-129949	Sequence 129949,
42	c	35	85.4	1885	18	US-10-437-963-75512	Sequence 75512, A
43	c	35	85.4	1901	17	US-10-424-599-131648	Sequence 131648,
44		35	85.4	1928	17	US-10-425-114-24113	Sequence 24113, A
45	c	35	85.4	2047	17	US-10-425-114-27013	Sequence 27013, A

ALIGNMENTS

RESULT 1
US-10-826-157-5
; Sequence 5, Application US/10826157
; Publication No. US20050064548A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist, Susan L.
; APPLICANT: Outeiro, Tiago
; TITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
; TITLE OF INVENTION: PROCESSED PROTEINS AND USES THEREFOR
; FILE REFERENCE: 17481-003001
; CURRENT APPLICATION NUMBER: US/10/826,157
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/472,317
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 60/463,284
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 384

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-826-157-5

Alignment Scores:

Pred. No.:	20.2	Length:	384
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-826-157-5 (1-384)

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Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
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Db        358 GAGGAGGCCCAGAGTGGGGGAGAC 381
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RESULT 2
US-09-925-298-172
; Sequence 172, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-298-172

Alignment Scores:

Pred. No.:	24.4	Length:	478
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-925-298-172 (1-478)

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Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
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Db        149 GAGGAGGCCCAGAGTGGGGGAGAC 172
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RESULT 3
US-10-102-806-172
; Sequence 172, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-806-172

Alignment Scores:

Pred. No.:	24.4	Length:	478
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-102-806-172 (1-478)

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Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
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Db        149 GAGGAGGCCCAGAGTGGGGGAGAC 172
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RESULT 4
US-09-918-995-2705
; Sequence 2705, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2705
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(479)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2705

Alignment Scores:

Pred. No.:	24.4	Length:	479
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-918-995-2705 (1-479)

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Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        371 GAGGAGGCCCAGAGTGGGGGAGAC 394
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RESULT 5
US-09-954-531-613
; Sequence 613, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20

```
;  PRIOR APPLICATION NUMBER: US/60/234,034
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,509
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US/60/234,567
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 1392
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 613
;   LENGTH: 550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-531-613

Alignment Scores:
Pred. No.:                27.5          Length:          550
Score:                    41.00         Matches:         8
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       9             Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-954-531-613 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 6
US-10-453-478-1
; Sequence 1, Application US/10453478
; Publication No. US20030208043A1
;   GENERAL INFORMATION:
;        APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                   Jian Ni and Jing-Shan Hu
;        TITLE OF INVENTION: Human Genes, Sequences and
;                            Expression Products
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                        CECCHI, STEWART & OLSTEIN
;             STREET: 6 BECKER FARM ROAD
;             CITY: ROSELAND
;             STATE: NEW JERSEY
;             COUNTRY: USA
;             ZIP: 07068
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 INCH DISKETTE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: MS-DOS
;             SOFTWARE: WORD PERFECT 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/453,478
;             FILING DATE: 04-Jun-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/705,771
;             FILING DATE: August 30, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MULLINS, J.G.
;             REGISTRATION NUMBER: 33,073
;             REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 973-994-1700
;             TELEFAX: 973-994-1744
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 550 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-453-478-1

Alignment Scores:
Pred. No.:                27.5          Length:          550
Score:                    41.00         Matches:         8
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       17            Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-453-478-1 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 7
US-10-843-641A-1680
; Sequence 1680, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;  APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US/09/954,531
;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1680
;   LENGTH: 550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-843-641A-1680

Alignment Scores:
Pred. No.:                27.5          Length:          550
Score:                    41.00         Matches:         8
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       19            Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-843-641A-1680 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 8
US-10-097-340-297
; Sequence 297, Application US/10097340
```

; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-297

Alignment Scores:

Pred. No.:	34.8	Length:	720
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-097-340-297 (1-720)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429
```

RESULT 9
US-10-282-174-469
; Sequence 469, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 469
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 30,57,85,243,250,377,512,531,555,561,672
; OTHER INFORMATION: N is any
US-10-282-174-469

Alignment Scores:

Pred. No.:	34.8	Length:	720
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-282-174-469 (1-720)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429
```

RESULT 10
US-10-600-009-469
; Sequence 469, Application US/10600009
; Publication No. US20050009031A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308B
; CURRENT APPLICATION NUMBER: US/10/600,009
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363

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;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/337,052
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/368,919
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 10/282,174
;  PRIOR FILING DATE: 2002-10-25
;  NUMBER OF SEQ ID NOS: 564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 469
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 30,57,85,243,250,377,512,531,555,561,672
;   OTHER INFORMATION: N is any
US-10-600-009-469

Alignment Scores:
Pred. No.:              34.8          Length:          720
Score:                  41.00         Matches:         8
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     19            Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-600-009-469 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 11
US-09-925-298-171
; Sequence 171, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103
;  CURRENT APPLICATION NUMBER: US/09/925,298
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 796
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-298-171

Alignment Scores:
Pred. No.:              37.9          Length:          796
Score:                  41.00         Matches:         8
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     9             Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-925-298-171 (1-796)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        466 GAGGAGGCCCAGAGTGGGGGAGAC 489

RESULT 12
US-10-102-806-171
; Sequence 171, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 796
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-102-806-171

Alignment Scores:
Pred. No.:              37.9          Length:          796
Score:                  41.00         Matches:         8
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     14            Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-102-806-171 (1-796)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        466 GAGGAGGCCCAGAGTGGGGGAGAC 489

RESULT 13
US-10-369-493-33286/c
; Sequence 33286, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 33286
;   LENGTH: 1125
;   TYPE: DNA
;   ORGANISM: Desulfitobacterium hafniense
US-10-369-493-33286

Alignment Scores:
Pred. No.:              201           Length:          1125
Score:                  38.00         Matches:         7
Percent Similarity:     100.00%       Conservative:    1
Best Local Similarity:  87.50%        Mismatches:      0
Query Match:            92.68%        Indels:          0
DB:                     17            Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-369-493-33286 (1-1125)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||:::||||||||
Db        609 GAAGAAGCCCAGGCCGGTGGCGAC 586

RESULT 14
```

US-10-425-115-90466/c
; Sequence 90466, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 90466
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(442)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_182507C.1
US-10-425-115-90466

Alignment Scores:

Pred. No.:	142	Length:	442
Score:	37.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	87.50%	Mismatches:	0
Query Match:	90.24%	Indels:	0
DB:	18	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-425-115-90466 (1-442)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              |||||||||:::|||||||||||
Db         55 GAGGAGGCGAGGAGCGGAGGGGAC 32
```

RESULT 15
US-10-437-963-8217
; Sequence 8217, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 8217
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14742C.1
US-10-437-963-8217

Alignment Scores:

Pred. No.:	564	Length:	2185
Score:	37.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	90.24%	Indels:	0
DB:	18	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-10-437-963-8217 (1-2185)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              |||||||||||   |||||||||
Db       1208 GAGGAAGCTCAGGAAGGAGGTGAC 1231
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Search completed: May 4, 2005, 16:39:46
Job time : 68.7405 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:55 ; Search time 18.5235 Seconds
(without alignments)
706.682 Million cell updates/sec

Title: US-09-017-715A-2_COPY_120_127
Perfect score: 41
Sequence: 1 EEAQSGGD 8

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100745_25632/app_query.fasta_1.661
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_@CGN_1_1_116_@runat_04052005_100745_25632 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		41	100.0	550	3	US-08-705-771-1	Sequence 1, Appli
2		41	100.0	550	4	US-09-417-540-1	Sequence 1, Appli
3		41	100.0	702	4	US-09-949-016-1915	Sequence 1915, Ap
4		41	100.0	720	4	US-09-949-016-442	Sequence 442, App
c 5		36	87.8	1902	4	US-09-949-016-5550	Sequence 5550, Ap
c 6		36	87.8	4985	3	US-09-473-717-1	Sequence 1, Appli
c 7		36	87.8	4985	4	US-09-949-016-152	Sequence 152, App
c 8		36	87.8	5515	3	US-09-398-193-98	Sequence 98, Appl
c 9		36	87.8	112114	4	US-09-949-016-17292	Sequence 17292, A
c 10		36	87.8	126200	4	US-09-949-016-11824	Sequence 11824, A
c 11		36	87.8	126200	4	US-09-949-016-13193	Sequence 13193, A
c 12		36	87.8	154605	4	US-09-949-016-11894	Sequence 11894, A
c 13		35	85.4	83708	4	US-09-949-016-17207	Sequence 17207, A
c 14		34	82.9	601	4	US-09-949-016-49739	Sequence 49739, A
15		34	82.9	628	3	US-09-328-111-367	Sequence 367, App
16		34	82.9	1653	4	US-09-830-111E-1	Sequence 1, Appli
c 17		34	82.9	29717	4	US-09-949-016-16284	Sequence 16284, A
c 18		34	82.9	60376	4	US-09-949-016-12423	Sequence 12423, A
c 19		33	80.5	204	4	US-09-621-976-18715	Sequence 18715, A
c 20		33	80.5	210	4	US-09-621-976-18727	Sequence 18727, A
c 21		33	80.5	219	4	US-09-621-976-18782	Sequence 18782, A
c 22		33	80.5	229	4	US-09-621-976-18788	Sequence 18788, A
c 23		33	80.5	361	4	US-09-621-976-18728	Sequence 18728, A
c 24		33	80.5	404	4	US-09-621-976-18769	Sequence 18769, A
25		33	80.5	431	4	US-09-513-999C-13044	Sequence 13044, A
c 26		33	80.5	450	4	US-09-621-976-3667	Sequence 3667, Ap
27		33	80.5	480	4	US-09-270-767-6338	Sequence 6338, Ap
28		33	80.5	480	4	US-09-270-767-21620	Sequence 21620, A
c 29		33	80.5	487	4	US-09-621-976-18762	Sequence 18762, A
c 30		33	80.5	495	4	US-09-621-976-3659	Sequence 3659, Ap
31		33	80.5	601	4	US-09-949-016-26549	Sequence 26549, A
32		33	80.5	601	4	US-09-949-016-26550	Sequence 26550, A
c 33		33	80.5	601	4	US-09-949-016-27764	Sequence 27764, A
34		33	80.5	601	4	US-09-949-016-65608	Sequence 65608, A
35		33	80.5	601	4	US-09-949-016-65609	Sequence 65609, A
36		33	80.5	601	4	US-09-949-016-164928	Sequence 164928,
c 37		33	80.5	601	4	US-09-949-016-202311	Sequence 202311,
c 38		33	80.5	670	3	US-09-404-879A-156	Sequence 156, App
c 39		33	80.5	670	4	US-09-338-933-156	Sequence 156, App
c 40		33	80.5	670	4	US-09-215-681-156	Sequence 156, App
c 41		33	80.5	670	4	US-09-216-003A-156	Sequence 156, App
c 42		33	80.5	670	4	US-09-667-857-156	Sequence 156, App
43		33	80.5	978	4	US-09-248-796A-5309	Sequence 5309, Ap
44		33	80.5	1005	4	US-09-270-767-26942	Sequence 26942, A
45		33	80.5	1208	4	US-09-270-767-25543	Sequence 25543, A

ALIGNMENTS

RESULT 1
US-08-705-771-1
; Sequence 1, Application US/08705771
; Patent No. 6054289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,771
; FILING DATE: August 30, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```
;      LENGTH:  550 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-705-771-1

Alignment Scores:
Pred. No.:                9.29          Length:         550
Score:                    41.00         Matches:        8
Percent Similarity:       100.00%       Conservative:   0
Best Local Similarity:    100.00%       Mismatches:     0
Query Match:              100.00%       Indels:         0
DB:                       3             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x US-08-705-771-1 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 2
US-09-417-540-1
; Sequence 1, Application US/09417540
; Patent No. 6639052
;   GENERAL INFORMATION:
;        APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                   Jian Ni and Jing-Shan Hu
;        TITLE OF INVENTION: Human Genes, Sequences and
;                            Expression Products
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                        CECCHI, STEWART & OLSTEIN
;             STREET: 6 BECKER FARM ROAD
;             CITY: ROSELAND
;             STATE: NEW JERSEY
;             COUNTRY: USA
;             ZIP: 07068
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 INCH DISKETTE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: MS-DOS
;             SOFTWARE: WORD PERFECT 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/417,540
;             FILING DATE: 14-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/705,771
;             FILING DATE: August 30, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MULLINS, J.G.
;             REGISTRATION NUMBER: 33,073
;             REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 973-994-1700
;             TELEFAX: 973-994-1744
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 550 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-417-540-1

Alignment Scores:
Pred. No.:                9.29          Length:         550
Score:                    41.00         Matches:        8
Percent Similarity:       100.00%       Conservative:   0
Best Local Similarity:    100.00%       Mismatches:     0
Query Match:              100.00%       Indels:         0
DB:                       4             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-417-540-1 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 3
US-09-949-016-1915
; Sequence 1915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1915
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1915

Alignment Scores:
Pred. No.:                12.1          Length:         702
Score:                    41.00         Matches:        8
Percent Similarity:       100.00%       Conservative:   0
Best Local Similarity:    100.00%       Mismatches:     0
Query Match:              100.00%       Indels:         0
DB:                       4             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-1915 (1-702)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        405 GAGGAGGCCCAGAGTGGGGGAGAC 428

RESULT 4
US-09-949-016-442
; Sequence 442, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 442
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-442
```

```
Alignment Scores:
Pred. No.:                12.4          Length:          720
Score:                    41.00         Matches:         8
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-442 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 5
US-09-949-016-5550/c
; Sequence 5550, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5550
;   LENGTH: 1902
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5550

Alignment Scores:
Pred. No.:                366           Length:          1902
Score:                    36.00         Matches:         7
Percent Similarity:       87.50%        Conservative:    0
Best Local Similarity:    87.50%        Mismatches:      1
Query Match:              87.80%        Indels:          0
DB:                       4             Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-5550 (1-1902)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||   |||||||||
Db        477 GAGGAAGCACAGCGCGGGGGCGAC 454

RESULT 6
US-09-473-717-1/c
; Sequence 1, Application US/09473717
; Patent No. 6372475
; GENERAL INFORMATION:
;  APPLICANT:  Storm, Daniel R.
;  APPLICANT:  Hacker, Beth
;  APPLICANT:  Tomlinson, James E.
;  APPLICANT:  COR Therapeutics, Inc.
;  APPLICANT:  University of Washington
;  TITLE OF INVENTION:  CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
;  TITLE OF INVENTION:  CYCLASE
;  FILE REFERENCE:  44481-5029-01-US
;  CURRENT APPLICATION NUMBER: US/09/473,717
;  CURRENT FILING DATE:  1999-12-29
;  PRIOR APPLICATION NUMBER:  PCT/US98/13541
;  PRIOR FILING DATE:  1998-07-01
;  PRIOR APPLICATION NUMBER:  60/098,559
;  PRIOR FILING DATE:  1997-07-01
;  PRIOR APPLICATION NUMBER:  08/886,440
;  PRIOR FILING DATE:  1997-07-01
;  NUMBER OF SEQ ID NOS:  3
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 4985
;   TYPE: DNA
;   ORGANISM: human type IX adenylyl cyclase
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (17)..(3898)
US-09-473-717-1

Alignment Scores:
Pred. No.:                1.04e+03      Length:          4985
Score:                    36.00         Matches:         7
Percent Similarity:       87.50%        Conservative:    0
Best Local Similarity:    87.50%        Mismatches:      1
Query Match:              87.80%        Indels:          0
DB:                       3             Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-473-717-1 (1-4985)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||   |||||||||
Db        475 GAGGAAGCACAGCGCGGGGGCGAC 452

RESULT 7
US-09-949-016-152/c
; Sequence 152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 152
;   LENGTH: 4985
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-152

Alignment Scores:
Pred. No.:                1.04e+03      Length:          4985
Score:                    36.00         Matches:         7
Percent Similarity:       87.50%        Conservative:    0
Best Local Similarity:    87.50%        Mismatches:      1
Query Match:              87.80%        Indels:          0
DB:                       4             Gaps:            0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-152 (1-4985)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||   |||||||||
Db        475 GAGGAAGCACAGCGCGGGGGCGAC 452

RESULT 8
US-09-398-193-98/c
; Sequence 98, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  TITLE OF INVENTION: Adenylate cyclase and uses therefor
;  FILE REFERENCE: P24360-
```

```
;  CURRENT APPLICATION NUMBER: US/09/398,193
;  CURRENT FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
;   LENGTH: 5515
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (539)..(4600)
US-09-398-193-98

Alignment Scores:
Pred. No.:              1.16e+03        Length:         5515
Score:                  36.00           Matches:        7
Percent Similarity:     87.50%          Conservative:   0
Best Local Similarity:  87.50%          Mismatches:     1
Query Match:            87.80%          Indels:         0
DB:                     3               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-398-193-98 (1-5515)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||   |||||||||
Db        997 GAGGAAGCACAGCGCGGGGGCGAC 974

RESULT 9
US-09-949-016-17292/c
; Sequence 17292, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17292
;   LENGTH: 112114
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17292

Alignment Scores:
Pred. No.:              2.98e+04        Length:         112114
Score:                  36.00           Matches:        7
Percent Similarity:     87.50%          Conservative:   0
Best Local Similarity:  87.50%          Mismatches:     1
Query Match:            87.80%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-17292 (1-112114)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||   |||||||||
Db       2477 GAGGAAGCACAGCGCGGGGGCGAC 2454

RESULT 10
US-09-949-016-11824/c
; Sequence 11824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11824
;   LENGTH: 126200
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(126200)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11824

Alignment Scores:
Pred. No.:              3.39e+04        Length:         126200
Score:                  36.00           Matches:        7
Percent Similarity:     87.50%          Conservative:   0
Best Local Similarity:  87.50%          Mismatches:     1
Query Match:            87.80%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-11824 (1-126200)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              |||||||||   ||||||||||||
Db     110246 GAGGAGGCACACAGTGGGGGGGAT 110223

RESULT 11
US-09-949-016-13193/c
; Sequence 13193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13193
;   LENGTH: 126200
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(126200)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13193

Alignment Scores:
Pred. No.:              3.39e+04        Length:         126200
Score:                  36.00           Matches:        7
Percent Similarity:     87.50%          Conservative:   0
Best Local Similarity:  87.50%          Mismatches:     1
Query Match:            87.80%          Indels:         0
DB:                     4               Gaps:           0
```

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-13193 (1-126200)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              |||||||||  ||||||||||||
Db     110246 GAGGAGGCACACAGTGGGGGGGAT 110223
```

RESULT 12
US-09-949-016-11894/c
; Sequence 11894, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11894
; LENGTH: 154605
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11894

Alignment Scores:

Pred. No.:	4.21e+04	Length:	154605
Score:	36.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	87.80%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-11894 (1-154605)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              |||||||||||  |||||||||
Db       2475 GAGGAAGCACAGCGCGGGGGCGAC 2452
```

RESULT 13
US-09-949-016-17207/c
; Sequence 17207, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17207
; LENGTH: 83708
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17207

Alignment Scores:

Pred. No.:	3.46e+04	Length:	83708
Score:	35.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.37%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-17207 (1-83708)

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Qy          1 GluGluAlaGlnSerGlyGly 7
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RESULT 14
US-09-949-016-49739/c
; Sequence 49739, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49739
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49739

Alignment Scores:

Pred. No.:	268	Length:	601
Score:	34.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	82.93%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-949-016-49739 (1-601)

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Db         56 GAGGTTGCACAGAGTGGGGGGGAT 33
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RESULT 15
US-09-328-111-367
; Sequence 367, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801

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;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 367
;    LENGTH: 628
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(628)
;    OTHER INFORMATION: n = A,T,C or G
US-09-328-111-367

Alignment Scores:
Pred. No.:                281             Length:         628
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Percent Similarity:       87.50%          Conservative:   1
Best Local Similarity:    75.00%          Mismatches:     1
Query Match:              82.93%          Indels:         0
DB:                       3               Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x US-09-328-111-367 (1-628)

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Search completed: May  4, 2005, 09:43:33
Job time : 63.5235 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 10:17:21 ; Search time 1033.05 Seconds
(without alignments)
748.404 Million cell updates/sec

Title: US-09-017-715A-2
Perfect score: 610
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
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-MAXLEN=2000000000 -USER=US09017715_@CGN_1_1_684_@runat_04052005_100747_25719
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Database : Published_Applications_NA:*
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	610	100.0	550	9	US-09-954-531-613	Sequence 613, App
2	610	100.0	550	17	US-10-453-478-1	Sequence 1, Appli
3	610	100.0	550	19	US-10-843-641A-1680	Sequence 1680, Ap
4	602	98.7	796	9	US-09-925-298-171	Sequence 171, App
5	602	98.7	796	14	US-10-102-806-171	Sequence 171, App
6	595	97.5	384	19	US-10-826-157-5	Sequence 5, Appli
7	595	97.5	720	14	US-10-097-340-297	Sequence 297, App
8	592	97.0	720	17	US-10-282-174-469	Sequence 469, App
9	592	97.0	720	19	US-10-600-009-469	Sequence 469, App
10	538	88.2	479	10	US-09-918-995-2705	Sequence 2705, Ap
11	468.5	76.8	786	14	US-10-267-849-1	Sequence 1, Appli
12	328	53.8	210	18	US-10-204-337A-5	Sequence 5, Appli
13	316	51.8	1018	17	US-10-152-319A-1710	Sequence 1710, Ap
14	316	51.8	1018	19	US-10-486-706-260	Sequence 260, App
15	312.5	51.2	437	18	US-10-737-262-2	Sequence 2, Appli
16	307.5	50.4	423	14	US-10-077-584-1	Sequence 1, Appli
17	307.5	50.4	423	18	US-10-204-337A-3	Sequence 3, Appli
18	307.5	50.4	423	19	US-10-826-157-1	Sequence 1, Appli
19	307.5	50.4	437	18	US-10-737-262-1	Sequence 1, Appli
20	307.5	50.4	1105	15	US-10-223-978-10	Sequence 10, Appl
21	307.5	50.4	1466	15	US-10-101-510-362	Sequence 362, App
22	307.5	50.4	1543	18	US-10-721-693-14	Sequence 14, Appl
23	307.5	50.4	1543	18	US-10-852-997-14	Sequence 14, Appl
24	304.5	49.9	755	17	US-10-112-944-11	Sequence 11, Appl
25	304	49.8	441	9	US-09-960-352-12619	Sequence 12619, A
26	304	49.8	453	9	US-09-960-352-5029	Sequence 5029, Ap
27	303.5	49.8	1096	10	US-09-921-406C-35	Sequence 35, Appl
28	303.5	49.8	1096	18	US-10-721-693-23	Sequence 23, Appl
29	303.5	49.8	1096	18	US-10-852-997-23	Sequence 23, Appl
30	302	49.5	405	19	US-10-826-157-3	Sequence 3, Appli
31	253	41.5	249	18	US-10-204-337A-4	Sequence 4, Appli
32	243	39.8	424	9	US-09-960-352-1978	Sequence 1978, Ap
33	233	38.2	473	10	US-09-918-995-1832	Sequence 1832, Ap
34	205	33.6	456	10	US-09-918-995-26977	Sequence 26977, A
35	202	33.1	393	9	US-09-960-352-3369	Sequence 3369, Ap
36	201.5	33.0	4606	17	US-10-240-425-388	Sequence 388, App
37	201.5	33.0	5666	17	US-10-282-174-72	Sequence 72, Appl
38	201.5	33.0	5666	19	US-10-600-009-72	Sequence 72, Appl
39	201.5	33.0	6012	17	US-10-282-174-483	Sequence 483, App
40	201.5	33.0	6012	19	US-10-600-009-483	Sequence 483, App
c 41	199	32.6	132	16	US-10-029-386-25796	Sequence 25796, A
c 42	199	32.6	502	16	US-10-029-386-12096	Sequence 12096, A
43	197.5	32.4	5666	17	US-10-282-174-73	Sequence 73, Appl
44	197.5	32.4	5666	19	US-10-600-009-73	Sequence 73, Appl
c 45	195	32.0	521	16	US-10-029-386-9757	Sequence 9757, Ap

ALIGNMENTS

RESULT 1
US-09-954-531-613
; Sequence 613, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567

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;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 1392
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 613
;   LENGTH: 550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-531-613

Alignment Scores:
Pred. No.:              2.15e-60        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-017-715A-2 (1-127) x US-09-954-531-613 (1-550)

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Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 2
US-10-453-478-1
; Sequence 1, Application US/10453478
; Publication No. US20030208043A1
;   GENERAL INFORMATION:
;        APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                   Jian Ni and Jing-Shan Hu
;        TITLE OF INVENTION: Human Genes, Sequences and
;                            Expression Products
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                        CECCHI, STEWART & OLSTEIN
;             STREET: 6 BECKER FARM ROAD
;             CITY: ROSELAND
;             STATE: NEW JERSEY
;             COUNTRY: USA
;             ZIP: 07068
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 INCH DISKETTE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: MS-DOS
;             SOFTWARE: WORD PERFECT 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/453,478
;             FILING DATE: 04-Jun-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/705,771
;             FILING DATE: August 30, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MULLINS, J.G.
;             REGISTRATION NUMBER: 33,073
;             REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 973-994-1700
;             TELEFAX: 973-994-1744
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 550 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-453-478-1

Alignment Scores:
Pred. No.:              2.15e-60        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     17              Gaps:           0

US-09-017-715A-2 (1-127) x US-10-453-478-1 (1-550)

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Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 3
US-10-843-641A-1680
; Sequence 1680, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;  APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US/09/954,531
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;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1680
;   LENGTH: 550
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-843-641A-1680

Alignment Scores:
Pred. No.:                2.15e-60        Length:         550
Score:                    610.00          Matches:        127
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       19              Gaps:           0

US-09-017-715A-2 (1-127) x US-10-843-641A-1680 (1-550)

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Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 4
US-09-925-298-171
; Sequence 171, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103
;  CURRENT APPLICATION NUMBER: US/09/925,298
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 796
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-298-171

Alignment Scores:
Pred. No.:                2.87e-59        Length:         796
Score:                    602.00          Matches:        125
Percent Similarity:       100.00%         Conservative:   2
Best Local Similarity:    98.43%          Mismatches:     0
Query Match:              98.69%          Indels:         0
DB:                       9               Gaps:           0

US-09-017-715A-2 (1-127) x US-09-925-298-171 (1-796)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        109 ATGGATGTYTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 168

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 228

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 288

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 348

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 408

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 468

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||||
Db        469 GAGGCCCAGAGTGGGGGAGAC 489

RESULT 5
US-10-102-806-171
; Sequence 171, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
;   LENGTH: 796
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

US-10-102-806-171

Alignment Scores:

Pred. No.:	2.87e-59	Length:	796
Score:	602.00	Matches:	125
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.43%	Mismatches:	0
Query Match:	98.69%	Indels:	0
DB:	14	Gaps:	0

US-09-017-715A-2 (1-127) x US-10-102-806-171 (1-796)

```
Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        109 ATGGATGTYTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 168

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 228

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 288

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        289 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 348

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 408

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 468

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        469 GAGGCCCAGAGTGGGGGAGAC 489
```

RESULT 6
US-10-826-157-5
; Sequence 5, Application US/10826157
; Publication No. US20050064548A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist, Susan L.
; APPLICANT: Outeiro, Tiago
; TITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
; TITLE OF INVENTION: PROCESSED PROTEINS AND USES THEREFOR
; FILE REFERENCE: 17481-003001
; CURRENT APPLICATION NUMBER: US/10/826,157
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/472,317
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 60/463,284
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-826-157-5

Alignment Scores:

Pred. No.:	6.95e-59	Length:	384
Score:	595.00	Matches:	124
Percent Similarity:	99.21%	Conservative:	2
Best Local Similarity:	97.64%	Mismatches:	1
Query Match:	97.54%	Indels:	0
DB:	19	Gaps:	0

US-09-017-715A-2 (1-127) x US-10-826-157-5 (1-384)

```
Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db          1 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 60

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 120

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 180

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 240

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 300

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 360

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        361 GAGGCCCAGAGTGGGGGAGAC 381
```

RESULT 7
US-10-097-340-297
; Sequence 297, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 720

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-097-340-297

Alignment Scores:
Pred. No.:              1.59e-58        Length:         720
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     14              Gaps:           0

US-09-017-715A-2 (1-127) x US-10-097-340-297 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         49 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 8
US-10-282-174-469
; Sequence 469, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
;  APPLICANT: Becker, Kenneth David
;  APPLICANT:  Velicelebi, Gonul
;  APPLICANT:  Elliot, Kathryn J.
;  APPLICANT:  Wang, Xin
;  APPLICANT:  Tanzi, Rudolph E.
;  APPLICANT:  Bertram, Lars
;  APPLICANT:  Saunders, Aleister J.
;  APPLICANT:  Mullin, Kristina M.
;  APPLICANT:  Sampson, Andrew Johnson
;  APPLICANT:  Blacker, Deborah Lynne
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
;  TITLE OF INVENTION:  ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
;  TITLE OF INVENTION:  NEURODEGENERATIVE DISEASES
;  FILE REFERENCE: 37481-3308
;  CURRENT APPLICATION NUMBER: US/10/282,174
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: US 60/339,525
;  PRIOR FILING DATE: 2001-10-25
;  PRIOR APPLICATION NUMBER: US 60/338,010
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/336,929
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/338,363
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/337,052
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/368,919
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 469
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 30,57,85,243,250,377,512,531,555,561,672
;   OTHER INFORMATION: N is any
US-10-282-174-469

Alignment Scores:
Pred. No.:              3.5e-58         Length:         720
Score:                  592.00          Matches:        124
Percent Similarity:     97.64%          Conservative:   0
Best Local Similarity:  97.64%          Mismatches:     3
Query Match:            97.05%          Indels:         0
DB:                     17              Gaps:           0

US-09-017-715A-2 (1-127) x US-10-282-174-469 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db         49 ATGGATGTNTTCAAGAAGGGCTTCTCCATCGCCAAGNAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCNGTGAGCNAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGNGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 9
US-10-600-009-469
; Sequence 469, Application US/10600009
; Publication No. US20050009031A1
; GENERAL INFORMATION:
;  APPLICANT: Becker, Kenneth David
;  APPLICANT:  Velicelebi, Gonul
;  APPLICANT:  Elliot, Kathryn J.
;  APPLICANT:  Wang, Xin
;  APPLICANT:  Tanzi, Rudolph E.
;  APPLICANT:  Bertram, Lars
;  APPLICANT:  Saunders, Aleister J.
;  APPLICANT:  Mullin, Kristina M.
;  APPLICANT:  Sampson, Andrew Johnson
;  APPLICANT:  Blacker, Deborah Lynne
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
;  TITLE OF INVENTION:  ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
;  TITLE OF INVENTION:  NEURODEGENERATIVE DISEASES
;  FILE REFERENCE: 37481-3308B
;  CURRENT APPLICATION NUMBER: US/10/600,009
;  CURRENT FILING DATE:  2003-06-18
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;  PRIOR APPLICATION NUMBER: US 60/339,525
;  PRIOR FILING DATE: 2001-10-25
;  PRIOR APPLICATION NUMBER: US 60/338,010
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/336,929
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/338,363
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/337,052
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/368,919
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 10/282,174
;  PRIOR FILING DATE: 2002-10-25
;  NUMBER OF SEQ ID NOS: 564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 469
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 30,57,85,243,250,377,512,531,555,561,672
;   OTHER INFORMATION: N is any
US-10-600-009-469

Alignment Scores:
Pred. No.:              3.5e-58       Length:          720
Score:                  592.00        Matches:         124
Percent Similarity:     97.64%        Conservative:    0
Best Local Similarity:  97.64%        Mismatches:      3
Query Match:            97.05%        Indels:          0
DB:                     19            Gaps:            0

US-09-017-715A-2 (1-127) x US-10-600-009-469 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db         49 ATGGATGTNTTCAAGAAGGGCTTCTCCATCGCCAAGNAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCNGTGAGCNAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGNGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 10
US-09-918-995-2705
; Sequence 2705, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2705
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(479)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2705

Alignment Scores:
Pred. No.:              3.03e-52      Length:          479
Score:                  538.00        Matches:         112
Percent Similarity:     99.14%        Conservative:    3
Best Local Similarity:  96.55%        Mismatches:      1
Query Match:            88.20%        Indels:          0
DB:                     10            Gaps:            0

US-09-017-715A-2 (1-127) x US-09-918-995-2705 (1-479)

Qy         12 LysLysGlyValValGlyAlaValGluLysThrLysGlnGlyValThrGluAlaAlaGlu 31
              ::::::||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db         47 CAGGAGGGCGTGGNGGGTGCGGTGGAAAAGACCAAGCAGGGGGTGACGGAAGCAGCTGAG 106

Qy         32 LysThrLysGluGlyValMetTyrValGlyAlaLysThrLysGluAsnValValGlnSer 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 AAGACCAAGGAGGGGGTCATGTATGTGGGAGCCAAGACCAAGGAGAATGTTGTACAGAGC 166

Qy         52 ValThrSerValAlaGluLysThrLysGluGlnAlaAsnAlaValSerLysAlaValVal 71
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||
Db        167 GTGACCTCAGTGGCCGAGAAGACCAAGGAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTG 226

Qy         72 SerSerValAsnThrValAlaThrLysThrValGluGluAlaGluAsnIleAlaValThr 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 AGCAGCGTCAACACTGTGGCCACCAAGACCGTGGAGGAGGCGGAGAACATCGCGGTCACC 286

Qy         92 SerGlyValValArgLysGluAspLeuArgProSerAlaProGlnGlnGluGlyGluAla 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCGGGGTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAGGAGGGTGAGGCA 346

Qy        112 SerLysGluLysGluGluValAlaGluGluAlaGlnSerGlyGlyAsp 127
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 TCCAAAGAGAAAGAGGAAGTGGCAGAGGAGGCCCAGAGTGGGGGAGAC 394

RESULT 11
US-10-267-849-1
; Sequence 1, Application US/10267849
; Publication No. US20030087824A1
; GENERAL INFORMATION:
;  APPLICANT: Ji, Hongjun
;  APPLICANT:  Rosen, Craig A.
;  TITLE OF INVENTION: Breast Cancer Specific Gene 2
;  FILE REFERENCE: 1488.0810001
;  CURRENT APPLICATION NUMBER: US/10/267,849
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US/08/673,284
;  PRIOR FILING DATE: 1996-06-28
;  PRIOR APPLICATION NUMBER: US 60/000,602
;  PRIOR FILING DATE: 1995-06-30
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 786
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-267-849-1
```

```
Alignment Scores:
Pred. No.:              5.09e-44        Length:         786
Score:                  468.50          Matches:        111
Percent Similarity:     86.15%          Conservative:   1
Best Local Similarity:  85.38%          Mismatches:     15
Query Match:            76.80%          Indels:         4
DB:                     14              Gaps:           1

US-09-017-715A-2 (1-127) x US-10-267-849-1 (1-786)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         95 ATGGATGTYTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 154

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 214

Qy         41 GlyAlaLysThrLysGluAsn---Val-ValGlnSerValThrSerValAlaGluLysTh 59
              ||||||||||||||||||||   ||| |||||||||||||||||||||||||||||||
Db        215 GGAGCCAAGACCAAGGAGAATGTTGTATGTACAGAGCGTGACCTCAGTGGCCGAGAAGAC 274

Qy         59 rLysGluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaTh 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db        275 CAAGGAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTKTGGCCAC 334

Qy         79 rLysThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAs 99
              ||||||||||||||||||||||||||||||||   ||||||      ||||||||||||
Db        335 CAAGACCGTKGAGGAGGCGGAGAACATCGCGGTCAMCTCCGGGKTGKTGCGCAAGGAGGA 394

Qy         99 pLeuArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGlu-LysGluGluValA 119
              |   ||||||      ||||||||||||||||||||||||   |||               |
Db        395 YTTKAGGCCATY-TKCCCCCAACAGGAGGGTGAGGCATCMARAGARARGAKWGSAAGWGG 453

Qy        119 laGluGluAlaGlnSerGlyGlyAsp 127
              ||         ||||||||||||||
Db        454 CMRAKKRGGMSCAGAGTGGGGGAGAC 479

RESULT 12
US-10-204-337A-5
; Sequence 5, Application US/10204337A
; Publication No. US20040128706A1
; GENERAL INFORMATION:
;  APPLICANT: Masliah, Eliezer
;  TITLE OF INVENTION: Method for screening for Anti-Amyloidogenic Properties and Method
;  TITLE OF INVENTION:  Treatment of Neurodegenerative Disease
;  FILE REFERENCE: 6627-PC9014
;  CURRENT APPLICATION NUMBER: US/10/204,337A
;  CURRENT FILING DATE:  2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/183,571
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/07216
;  PRIOR FILING DATE: 2001-03-17
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-204-337A-5

Alignment Scores:
Pred. No.:              1.02e-28        Length:         210
Score:                  328.00          Matches:        68
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  97.14%          Mismatches:     0
Query Match:            53.77%          Indels:         0
DB:                     18              Gaps:           0

US-09-017-715A-2 (1-127) x US-10-204-337A-5 (1-210)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db          1 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 60

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 120

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 180

Qy         61 GluGlnAlaAsnAlaValSerLysAlaVal 70
              ||||||||||||||||||||:::||||||
Db        181 GAGCAGGCCAACGCGGTGAGCGAGGCTGTG 210

RESULT 13
US-10-152-319A-1710
; Sequence 1710, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Higgs, Brandon
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  TITLE OF INVENTION: Molecular Toxicology Modeling
;  FILE REFERENCE: 44921-5089-US
;  CURRENT APPLICATION NUMBER: US/10/152,319A
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: US 60/292,335
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/297,523
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,925
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,810
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,807
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,808
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/315,047
;  PRIOR FILING DATE: 2001-08-28
;  PRIOR APPLICATION NUMBER: US 60/324,928
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US 60/330,867
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/330,462
;  PRIOR FILING DATE: 2001-10-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2221
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1710
;   LENGTH: 1018
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. NM_019169
US-10-152-319A-1710

Alignment Scores:
Pred. No.:              1.91e-26        Length:         1018
Score:                  316.00          Matches:        70
Percent Similarity:     68.60%          Conservative:   13
Best Local Similarity:  57.85%          Mismatches:     32
Query Match:            51.80%          Indels:         6
DB:                     17              Gaps:           1

US-09-017-715A-2 (1-127) x US-10-152-319A-1710 (1-1018)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||   ||||||   |||   ||||||:::|||||||||   |||   |||
Db         28 ATGGATGTGTTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 87
```

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Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||   |||||||||   ||||||||||||||||||:::||||||
Db         88 AAAACCAAGCAGGGTGTGGCAGAGGCAGCTGGGAAGACAAAAGAGGGCGTCCTCTATGTA 147

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||||||||   ||||||     ||||||:::||||||||||||||||||
Db        148 GGTTCCAAAACTAAGGAGGGAGTCGTTCATGGAGTGACAACAGTGGCTGAGAAGACCAAA 207

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||          |||      |||||||||:::   |||      ||||||  |||
Db        208 GAGCAAGTGACAAATGTTGGAGGGGCAGTGGTGACTGGTGTGACAGCAGTCGCTCAGAAG 267

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              |||||||||   |||   |||||||||     :::|||   |||:::|||:::   :::
Db        268 ACAGTGGAGGGAGCTGGGAACATTGCTGCTGCCACTGGTTTTGTCAAGAAGGACCAGATG 327

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                                 :::||||||          :::|||   :::   |||
Db        328 ------------------GGCAAGGGTGAAGAAGGGTACCCACAAGAGGGAATCCTGGAA 369

Qy        121 Glu 121
              :::
Db        370 GAC 372
```

RESULT 14
US-10-486-706-260
; Sequence 260, Application US/10486706
; Publication No. US20050071088A1
; GENERAL INFORMATION:
; APPLICANT: LANDFIELD, PHILIP W.
; APPLICANT: BLALOCK, ERIC M.
; APPLICANT: CHEN, KUEY-CHU
; APPLICANT: FOSTER, THOMAS C.
; TITLE OF INVENTION: GENE EXPRESSION PROFILE BIOMARKERS AND THERAPEUTIC TARGETS FOR
; TITLE OF INVENTION: BRAIN AGING AND AGE-RELATED COGNITIVE IMPAIRMENT
; FILE REFERENCE: 50229-426
; CURRENT APPLICATION NUMBER: US/10/486,706
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: PCT/US02/25607
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 60/311,343
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 260
; LENGTH: 1018
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-486-706-260

Alignment Scores:

Pred. No.:	1.91e-26	Length:	1018
Score:	316.00	Matches:	70
Percent Similarity:	68.60%	Conservative:	13
Best Local Similarity:	57.85%	Mismatches:	32
Query Match:	51.80%	Indels:	6
DB:	19	Gaps:	1

US-09-017-715A-2 (1-127) x US-10-486-706-260 (1-1018)

```
Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||   ||||||   |||   ||||||:::|||||||||   |||   |||
Db         28 ATGGATGTGTTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 87

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||   |||||||||   ||||||||||||||||||:::||||||
Db         88 AAAACCAAGCAGGGTGTGGCAGAGGCAGCTGGGAAGACAAAAGAGGGCGTCCTCTATGTA 147

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||||||||   ||||||     ||||||:::||||||||||||||||||
Db        148 GGTTCCAAAACTAAGGAGGGAGTCGTTCATGGAGTGACAACAGTGGCTGAGAAGACCAAA 207
```

```
Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||          |||      |||||||||:::   |||      ||||||  |||
Db        208 GAGCAAGTGACAAATGTTGGAGGGGCAGTGGTGACTGGTGTGACAGCAGTCGCTCAGAAG 267

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              |||||||||   |||   |||||||||     :::|||   |||:::|||:::   :::
Db        268 ACAGTGGAGGGAGCTGGGAACATTGCTGCTGCCACTGGTTTTGTCAAGAAGGACCAGATG 327

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                                 :::||||||          :::|||   :::   |||
Db        328 ------------------GGCAAGGGTGAAGAAGGGTACCCACAAGAGGGAATCCTGGAA 369

Qy        121 Glu 121
              :::
Db        370 GAC 372
```

RESULT 15
US-10-737-262-2
; Sequence 2, Application US/10737262
; Publication No. US20040197315A1
; GENERAL INFORMATION:
; APPLICANT: Stefanis, Leonidas
; APPLICANT: Greene, Lloyd A.
; TITLE OF INVENTION: Dopaminergic Cell Lines Stably Expressing A53T Alpha-Synuclein
; TITLE OF INVENTION: and Methods of Using Same
; FILE REFERENCE: 5199-26
; CURRENT APPLICATION NUMBER: US/10/737,262
; CURRENT FILING DATE: 2003-12-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-262-2

Alignment Scores:

Pred. No.:	1.58e-26	Length:	437
Score:	312.50	Matches:	69
Percent Similarity:	71.82%	Conservative:	10
Best Local Similarity:	62.73%	Mismatches:	28
Query Match:	51.23%	Indels:	3
DB:	18	Gaps:	1

US-09-017-715A-2 (1-127) x US-10-737-262-2 (1-437)

```
Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||   ||||||   |||   ||||||:::|||||||||   |||   |||
Db         15 ATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 74

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||   |||||||||   ||||||||||||||||||:::||||||
Db         75 AAAACCAAACAGGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTTCTCTATGTA 134

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||||||||   ||||||     ||||||:::||||||||||||||||||
Db        135 GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGACAACAGTGGCTGAGAAGACCAAA 194

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||          |||      |||||||||:::   |||      ||||||  |||
Db        195 GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG 254

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              |||||||||   |||   :::||||||     :::|||   |||:::|||:::   |||
Db        255 ACAGTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG 314

Qy        101 ---------ArgProSerAlaProGlnGln 107
                          |||||||||:::
Db        315 GGCAAGAATGAAGAAGGAGCCCCACAGGAA 344
```

Search completed: May 4, 2005, 16:39:31
Job time : 1042.71 secs

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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:56 ; Search time 5778.07 Seconds
(without alignments)
836.639 Million cell updates/sec

Title: US-09-017-715A-2
Perfect score: 610
Sequence: 1 MDVFKKGFSIAKKGVVGAVE.....EGEASKEKEEVAEEAQSGGD 127

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100744_25619/app_query.fasta_1.661
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_@CGN_1_1_5334_@runat_04052005_100744_25619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	602	98.7	555	7	CV028548	CV028548 7090 Full
2	602	98.7	578	5	BP212912	BP212912 BP212912
3	602	98.7	582	5	BP197662	BP197662 BP197662
4	602	98.7	584	5	BP201686	BP201686 BP201686
5	602	98.7	653	4	BI757131	BI757131 603030894
6	602	98.7	751	4	BI836596	BI836596 603089575
7	602	98.7	781	5	BQ893395	BQ893395 AGENCOURT
8	602	98.7	809	5	BM921124	BM921124 AGENCOURT
9	602	98.7	855	5	BQ882072	BQ882072 AGENCOURT
10	602	98.7	884	5	BQ439430	BQ439430 AGENCOURT
11	602	98.7	891	5	BQ221776	BQ221776 AGENCOURT
12	602	98.7	903	4	BG286466	BG286466 602382954
13	595	97.5	558	4	BI548891	BI548891 603189023
14	595	97.5	568	4	BG708703	BG708703 602674249
15	595	97.5	617	4	BG707764	BG707764 602671103
16	595	97.5	659	7	CN410061	CN410061 170006001
17	595	97.5	755	4	BI597796	BI597796 603248669
18	595	97.5	824	4	BI600882	BI600882 603249209
19	591	96.9	765	4	BI603159	BI603159 603249801
20	591	96.9	768	4	BI603171	BI603171 603249815
21	589	96.6	937	5	BU157619	BU157619 AGENCOURT
22	589	96.6	1009	5	BU179779	BU179779 AGENCOURT
23	576	94.4	641	1	AL712443	AL712443 DKFZp686B
24	575	94.3	555	5	BX474500	BX474500 DKFZp686D
25	567	93.0	623	5	BP381244	BP381244 BP381244
26	566.5	92.9	799	4	BI488930	BI488930 603021641
27	564.5	92.5	949	5	BQ068800	BQ068800 AGENCOURT
28	557	91.3	706	4	BG328738	BG328738 602427017
29	555	91.0	583	5	BP200612	BP200612 BP200612
30	548	89.8	583	5	BP346497	BP346497 BP346497
31	542	88.9	756	5	BQ901053	BQ901053 AGENCOURT
32	541	88.7	489	5	BP201709	BP201709 BP201709
33	526	86.2	462	5	BX474511	BX474511 DKFZp686E
34	524	85.9	467	6	CB107161	CB107161 K-EST0145
35	523	85.7	511	2	AW659211	AW659211 96177 MAR
36	523	85.7	625	7	CR452251	CR452251 CR452251
37	523	85.7	625	7	CR454933	CR454933 CR454933
38	523	85.7	646	7	CR551748	CR551748 CR551748
39	523	85.7	670	7	CO879176	CO879176 BovGen_07
40	523	85.7	689	7	CR454179	CR454179 CR454179
c 41	523	85.7	700	7	CK770094	CK770094 958221 MA
42	523	85.7	801	7	CO873848	CO873848 BovGen_02
43	522.5	85.7	721	7	CN157077	CN157077 945748 MA
c 44	522.5	85.7	721	7	CN159030	CN159030 948052 MA
c 45	519	85.1	799	7	CO877016	CO877016 BovGen_05

ALIGNMENTS

RESULT 1
CV028548
LOCUS CV028548 555 bp mRNA linear EST 20-AUG-2004
DEFINITION 7090 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC014098, mRNA sequence.
ACCESSION CV028548
VERSION CV028548.1 GI:51486632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 555)
AUTHORS Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
TITLE Human ORFeome Version 1.1: a Platform for Reverse Proteomics
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers
PCR PRimers
FORWARD: ATGGATGTCTTCAAGAAGGGCTTCTC
BACKWARD: TAGTCTCCCCCACTCTGG

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                     /db_xref="taxon:9606"
                     /tissue_type="mixed"
                     /clone_lib="Full Length cDNA from the Mammalian Gene
                     Collection"
                     /note="Vector: mixed; The ORFs were PCR amplified from the
                     MGC (Mammalian Gene Collection) as of April 2004 and
                     cloned by recombinational Gateway cloning into pDONR223
                     Donor vector. Reference : MGC (Mammalian Gene Collection)
                     Program Team, Generation and Initial Analysis of more than
                     15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                     2002, 99(26), 16899-16903"
ORIGIN

Alignment Scores:
Pred. No.:              1.39e-58       Length:         555
Score:                  602.00         Matches:        125
Percent Similarity:     100.00%        Conservative:   2
Best Local Similarity:  98.43%         Mismatches:     0
Query Match:            98.69%         Indels:         0
DB:                     7              Gaps:           0

US-09-017-715A-2 (1-127) x CV028548 (1-555)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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Db          1 ATGGATGTCTTCAAAAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 60

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
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Db        301 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 360

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        361 GAGGCCCAGAGTGGGGGAGAC 381

RESULT 2
BP212912
LOCUS       BP212912                 578 bp    mRNA    linear   EST 15-SEP-2004
DEFINITION  BP212912 Sugano cDNA library, cerebrum Homo sapiens cDNA clone
            CBR05118, mRNA sequence.
ACCESSION   BP212912
VERSION     BP212912.1  GI:52085803
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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ORIGIN

Alignment Scores:
Pred. No.:              1.47e-58       Length:         578
Score:                  602.00         Matches:        125
Percent Similarity:     100.00%        Conservative:   2
Best Local Similarity:  98.43%         Mismatches:     0
Query Match:            98.69%         Indels:         0
DB:                     5              Gaps:           0

US-09-017-715A-2 (1-127) x BP212912 (1-578)

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Db        125 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 184

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Db        185 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 244

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        245 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 304

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Db        305 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 364

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Db        365 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 424

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
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Db        425 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 484

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        485 GAGGCCCAGAGTGGGGGAGAC 505

RESULT 3
BP197662
LOCUS       BP197662                 582 bp    mRNA    linear   EST 14-SEP-2004
DEFINITION  BP197662 Sugano cDNA library, adrenal gland Homo sapiens cDNA clone
            ADG06551, mRNA sequence.
ACCESSION   BP197662
VERSION     BP197662.1  GI:52043849
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
```

```
          Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE   Sequence comparison of human and mouse genes reveals a homologous
          block structure in the promoter regions
  JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:9606"
                    /clone="ADG06551"
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ORIGIN

Alignment Scores:
Pred. No.:              1.48e-58        Length:         582
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     5               Gaps:           0

US-09-017-715A-2 (1-127) x BP197662 (1-582)

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Db         85 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 144

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Db        145 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 204

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        205 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 264

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Db        265 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 324

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Db        325 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 384

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
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Db        385 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 444

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        445 GAGGCCCAGAGTGGGGGAGAC 465

RESULT 4
BP201686
LOCUS       BP201686                584 bp    mRNA    linear   EST 14-SEP-2004
DEFINITION  BP201686 Sugano cDNA library, amygdala Homo sapiens cDNA clone
            AMR06165, mRNA sequence.
ACCESSION   BP201686
VERSION     BP201686.1  GI:52051909
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES              Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.49e-58        Length:         584
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     5               Gaps:           0

US-09-017-715A-2 (1-127) x BP201686 (1-584)

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Db        125 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 184

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Db        185 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 244

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        245 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 304

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Db        305 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 364

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Db        365 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 424

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
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Db        425 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 484

Qy        121 GluAlaGlnSerGlyGlyAsp 127
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RESULT 5
BI757131
LOCUS       BI757131                653 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603030894F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5201062 5',
            mRNA sequence.
ACCESSION   BI757131
VERSION     BI757131.1  GI:15748709
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 653)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11503 row: l column: 23
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FEATURES Location/Qualifiers
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/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.72e-58	Length:	653
Score:	602.00	Matches:	125
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.43%	Mismatches:	0
Query Match:	98.69%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2 (1-127) x BI757131 (1-653)

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Db        117 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 176

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        177 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 236

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
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Qy        121 GluAlaGlnSerGlyGlyAsp 127
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Db        417 GAGGCCCAGAGTGGGGGAGAC 437
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RESULT 6
BI836596
LOCUS BI836596 751 bp mRNA linear EST 04-OCT-2001
DEFINITION 603089575F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5228538 5', mRNA sequence.
ACCESSION BI836596
VERSION BI836596.1 GI:15948146
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 751)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11575 row: e column: 19
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FEATURES Location/Qualifiers
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/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2.06e-58	Length:	751
Score:	602.00	Matches:	125
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.43%	Mismatches:	0
Query Match:	98.69%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2 (1-127) x BI836596 (1-751)

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Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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Db        216 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 275

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Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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Db        336 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 395

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 455
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Qy        121 GluAlaGlnSerGlyGlyAsp 127
              ||||||||||||||||||||
Db        456 GAGGCCCAGAGTGGGGGAGAC 476

RESULT 7
BQ893395
LOCUS       BQ893395                781 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8121065 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6178582 5', mRNA sequence.
ACCESSION   BQ893395
VERSION     BQ893395.1  GI:22285409
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13558  row: f  column: 23
            High quality sequence stop: 436.
FEATURES             Location/Qualifiers
     source          1. .781
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6178582"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              2.16e-58        Length:         781
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     5               Gaps:           0

US-09-017-715A-2 (1-127) x BQ893395 (1-781)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         71 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 130

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 190

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 250

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        251 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 310

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 370

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 430

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              ||||||||||||||||||||
Db        431 GAGGCCCAGAGTGGGGGAGAC 451

RESULT 8
BM921124
LOCUS       BM921124                809 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6633376 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752462
            5', mRNA sequence.
ACCESSION   BM921124
VERSION     BM921124.1  GI:19371503
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 809)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12786  row: k  column: 23
            High quality sequence stop: 738.
FEATURES             Location/Qualifiers
     source          1. .809
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5752462"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.26e-58        Length:         809
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     5               Gaps:           0
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US-09-017-715A-2 (1-127) x BM921124 (1-809)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        114 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 173

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 233

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 293

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        294 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 353

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 413

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 473

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        474 GAGGCCCAGAGTGGGGGAGAC 494

RESULT 9
BQ882072
LOCUS       BQ882072                855 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8586140 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6195522 5', mRNA sequence.
ACCESSION   BQ882072
VERSION     BQ882072.1  GI:22274080
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13602  row: h  column: 19
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
     source          1. .855
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6195522"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              2.43e-58      Length:          855
Score:                  602.00        Matches:         125
Percent Similarity:     100.00%       Conservative:    2
Best Local Similarity:  98.43%        Mismatches:      0
Query Match:            98.69%        Indels:          0
DB:                     5             Gaps:            0

US-09-017-715A-2 (1-127) x BQ882072 (1-855)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         94 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 153

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 213

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 273

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        274 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 333

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 393

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 453

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        454 GAGGCCCAGAGTGGGGGAGAC 474

RESULT 10
BQ439430
LOCUS       BQ439430                884 bp    mRNA    linear   EST 24-MAY-2002
DEFINITION  AGENCOURT_7911914 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6010114
            5', mRNA sequence.
ACCESSION   BQ439430
VERSION     BQ439430.1  GI:21178506
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13197  row: k  column: 11
            High quality sequence stop: 559.
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FEATURES             Location/Qualifiers
     source          1. .884
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6010114"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

Alignment Scores:
Pred. No.:              2.54e-58        Length:         884
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     5               Gaps:           0

US-09-017-715A-2 (1-127) x BQ439430 (1-884)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         94 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 153

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 213

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 273

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        274 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 333

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 393

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 453

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        454 GAGGCCCAGAGTGGGGGAGAC 474

RESULT 11
BQ221776
LOCUS       BQ221776                 891 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7549973 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6057784
            5', mRNA sequence.
ACCESSION   BQ221776
VERSION     BQ221776.1  GI:20403176
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 891)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13321  row: m  column: 17
            High quality sequence stop: 734.
FEATURES             Location/Qualifiers
     source          1. .891
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6057784"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
ORIGIN

Alignment Scores:
Pred. No.:              2.56e-58        Length:         891
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     5               Gaps:           0

US-09-017-715A-2 (1-127) x BQ221776 (1-891)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        118 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 177

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 237

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 297

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        298 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 357

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 417

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 477

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        478 GAGGCCCAGAGTGGGGGAGAC 498

RESULT 12
BG286466
LOCUS       BG286466                 903 bp    mRNA    linear   EST 21-FEB-2001
DEFINITION  602382954F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4500613 5',
            mRNA sequence.
ACCESSION   BG286466
VERSION     BG286466.1  GI:13039369
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
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  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10366  row: k  column: 14
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .903
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4500613"
                     /tissue_type="transitional cell papilloma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_93"
                     /note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.61e-58        Length:         903
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2 (1-127) x BG286466 (1-903)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         87 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 146

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 206

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 266

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        267 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 326

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 386

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 446

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||||
Db        447 GAGGCCCAGAGTGGGGGAGAC 467

RESULT 13
BI548891
LOCUS       BI548891                 558 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603189023F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5260589 5',
            mRNA sequence.

ACCESSION   BI548891
VERSION     BI548891.1  GI:15436203
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11656  row: m  column: 06
            High quality sequence stop: 558.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5260589"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this
                     is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              8.82e-58        Length:         558
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2 (1-127) x BI548891 (1-558)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        130 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 189

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 249

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 309

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        310 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 369

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 429
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Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        430 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 489

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        490 GAGGCCCAGAGTGGGGGAGAC 510

RESULT 14
BG708703
LOCUS       BG708703                568 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602674249F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4796820 5',
            mRNA sequence.
ACCESSION   BG708703
VERSION     BG708703.1  GI:13986308
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10682  row: a  column: 13
            High quality sequence stop: 566.
FEATURES             Location/Qualifiers
     source          1. .568
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4796820"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length  clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              9.02e-58        Length:         568
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2 (1-127) x BG708703 (1-568)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        108 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 167

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 227

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 287

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        288 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 347

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 407

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        408 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 467

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        468 GAGGCCCAGAGTGGGGGAGAC 488

RESULT 15
BG707764
LOCUS       BG707764                617 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602671103F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4793833 5',
            mRNA sequence.
ACCESSION   BG707764
VERSION     BG707764.1  GI:13984439
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10674  row: e  column: 02
            High quality sequence stop: 617.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4793833"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length  clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

Alignment Scores:
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Pred. No.:	1e-57	Length:	617
Score:	595.00	Matches:	124
Percent Similarity:	99.21%	Conservative:	2
Best Local Similarity:	97.64%	Mismatches:	1
Query Match:	97.54%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2 (1-127) x BG707764 (1-617)

```
Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         58 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 117

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 177

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 237

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        238 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 297

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 357

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        358 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 417

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        418 GAGGCCCAGAGTGGGGGAGAC 438
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Search completed: May 4, 2005, 13:46:32
Job time : 5788.07 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:52 ; Search time 58.4698 Seconds
(without alignments)
809.955 Million cell updates/sec

Title: US-09-017-715A-2_COPY_120_127
Perfect score: 41
Sequence: 1 EEAQSGGD 8

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100743_25600/app_query.fasta_1.661
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	478	3	AAF21785	Aaf21785 Human bre
2	41	100.0	479	9	ACH15493	Ach15493 Human adu
3	41	100.0	488	12	ADM66887	Adm66887 Human hom
4	41	100.0	550	2	AAV42669	Aav42669 Human bre
5	41	100.0	550	3	AAA39470	Aaa39470 Human HBG
6	41	100.0	550	6	ABL63343	Abl63343 Breast ca
7	41	100.0	550	6	ABV73813	Abv73813 Human gam
8	41	100.0	550	6	ABV73915	Abv73915 Human gam
9	41	100.0	550	10	AAD63568	Aad63568 Human amy
10	41	100.0	550	10	ADG47636	Adg47636 Human amy
11	41	100.0	720	2	AAX29997	Aax29997 Human per
12	41	100.0	720	6	ABS76519	Abs76519 cDNA enco
13	41	100.0	720	10	ADE43864	Ade43864 Human SNC
14	41	100.0	720	12	ADH54342	Adh54342 Human SNC
15	41	100.0	783	4	AAI93778	Aai93778 Human pol
16	41	100.0	796	3	AAF21784	Aaf21784 Human bre
17	41	100.0	990	13	ADR98806	Adr98806 Lung spec
c 18	38	92.7	1125	13	ADS57612	Ads57612 Bacterial
c 19	38	92.7	110000	11	ADM27081_11	Continuation (12 o
20	37	90.2	1275	4	ABL04107	Abl04107 Drosophil
c 21	37	90.2	3275	4	ABL04106	Abl04106 Drosophil
22	36	87.8	2116	10	ADB62945	Adb62945 Human cDN
23	36	87.8	3790	10	ADC39175	Adc39175 Novel hum
c 24	36	87.8	4062	13	ADQ89903	Adq89903 Antagonis
c 25	36	87.8	4949	12	ADQ85477	Adq85477 Human tum
c 26	36	87.8	4985	2	AAX00463	Aax00463 Human typ
c 27	36	87.8	4985	12	ADP21328	Adp21328 Gene ADCY
28	36	87.8	5054	10	ADF74204	Adf74204 Human nov
29	36	87.8	5236	10	ADC30279	Adc30279 Human nov
30	36	87.8	5372	12	ADQ25367	Adq25367 Human sof
c 31	36	87.8	349980	6	ABQ81847	Abq81847 Bifidobac
32	35	85.4	458	4	AAK76569	Aak76569 Human imm
33	35	85.4	458	4	AAK76570	Aak76570 Human imm
34	35	85.4	518	13	ACN48722	Acn48722 Cotton pr
c 35	35	85.4	547	12	ACH73352	Ach73352 Human gen
36	35	85.4	677	2	AAX04876	Aax04876 Human gam
c 37	35	85.4	918	13	ADT46476	Adt46476 Bacterial
c 38	35	85.4	1273	11	ACN91507	Acn91507 Breast ca
c 39	35	85.4	2143	10	ADC07759	Adc07759 Rice DNA
c 40	35	85.4	2154	10	ADC08252	Adc08252 Rice DNA
c 41	35	85.4	2251	10	ADI60540	Adi60540 Secreted
c 42	35	85.4	3081	4	ABL27575	Abl27575 Drosophil
c 43	35	85.4	4259	10	ADB58369	Adb58369 Toxicity-
c 44	35	85.4	4259	10	ADB52941	Adb52941 Primary r
c 45	35	85.4	4292	10	ADE71246	Ade71246 Novel hum

ALIGNMENTS

RESULT 1
AAF21785
ID AAF21785 standard; DNA; 478 BP.
XX
AC AAF21785;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 172.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS Homo sapiens.
XX
PN WO200055173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005881.
XX
PR 12-MAR-1999; 99US-0124270P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-611515/58.
DR P-PSDB; AAB58882.
XX
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention, treatment
PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT neurological diseases.
XX
PS Claim 1; Page 609; 1299pp; English.
XX
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC protein sequences are used in the diagnosis of cancer, particularly
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC and agonists may also be used in the diagnosis, prevention and treatment
CC of immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC cardiovascular disorders such as myocardial ischaemias; wound healing;
CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases
XX
SQ Sequence 478 BP; 118 A; 150 C; 113 G; 97 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	47.8	Length:	478
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x AAF21785 (1-478)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        149 GAGGAGGCCCAGAGTGGGGGAGAC 172
```

RESULT 2
ACH15493
ID ACH15493 standard; cDNA; 479 BP.
XX
AC ACH15493;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult brain cDNA #2705.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 2705; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 479 BP; 120 A; 118 C; 178 G; 56 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	47.9	Length:	479
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x ACH15493 (1-479)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        371 GAGGAGGCCCAGAGTGGGGGAGAC 394
```

RESULT 3
ADM66887
ID ADM66887 standard; DNA; 488 BP.
XX
AC ADM66887;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human homologue of murine adipocyte specific gamma synuclein DNA Seq 20.
XX
KW human; adipocyte specific; gene; ds; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; gamma synuclein.
XX
OS Homo sapiens.
XX
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.

XX
PR 29-JUL-2002; 2002US-0398785P.
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGE-) HMGENE INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR WPI; 2004-143846/14.
DR P-PSDB; ADM67167.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Claim 11; SEQ ID NO 20; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polynucleotide sequence is a human homologue
CC of a murine adipocyte specific DNA sequence of the invention.
XX
SQ Sequence 488 BP; 127 A; 119 C; 176 G; 66 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	48.9	Length:	488
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x ADM66887 (1-488)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 4
AAV42669
ID AAV42669 standard; cDNA; 550 BP.
XX
AC AAV42669;
XX
DT 09-NOV-1998 (first entry)
XX
DE Human breast cancer specific gene 1 (BCSG1) cDNA.
XX
KW Breast cancer specific gene 1; BCGS1; human; metastasis; diagnosis;
KW therapy; genetic marker; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12. .395
FT /*tag= a
XX
PN WO9833915-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US001804.
XX
PR 03-FEB-1997; 97US-0037080P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ji H, Rosen CA;
XX
DR WPI; 1998-446811/38.
DR P-PSDB; AAW63123.
XX
PT New isolated human breast cancer specific gene - used to develop products
PT for the diagnosis, clinical management and treatment of breast cancer and
PT metastases.
XX
PS Claim 4; Fig 1; 73pp; English.
XX
CC This cDNA clone corresponds to the transcript of the newly identified
CC human breast cancer specific gene 1 (BCSG1), and includes an open reading
CC frame for a 14.2 kDa protein (see AAW63123). It was isolated from a
CC breast cancer cDNA library following an EST search for novel genes
CC differentially expressed in breast cancer versus healthy breast tissue.
CC The clone is deposited at ATCC 97175 and ATCC 97856. A gradient and stage
CC -specific BCSG1 expression has been demonstrated from virtually no
CC detectable expression in normal or benign breast to low level and partial
CC expression in low grade in situ breast carcinoma and high expression in
CC infiltrating malignant breast carcinomas. BCSG1 is useful as a breast
CC cancer progression marker. Recombinant vectors and host cells useful for
CC recombinant production of BCSG1 polypeptides (including epitope- bearing
CC polypeptides) are provided. BCSG1 polynucleotides, polypeptides and
CC antibodies can be used for the detection of breast cancer cells or breast
CC cancer metastasis, and to develop methods for the clinical management and
CC treatment of breast cancer
XX
SQ Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	55.4	Length:	550
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x AAV42669 (1-550)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 5
AAA39470
ID AAA39470 standard; DNA; 550 BP.
XX
AC AAA39470;
XX
DT 24-AUG-2000 (first entry)
XX
DE Human HBGBA67A DNA.
XX
KW Human; ADA2; cytostatic; gene therapy; treatment; cancer;
KW amyloid-like protein; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12. .395
FT /*tag= a
FT /product= "HBGBA67"
XX

PN US6054289-A.
XX
PD 25-APR-2000.
XX
PF 30-AUG-1996; 96US-00705771.
XX
PR 30-AUG-1995; 95US-0002993P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA;
XX
DR WPI; 2000-338491/29.
DR P-PSDB; AAY87779.
XX
PT New polynucleotide encoding human AD2 is useful for treating cancer and
PT for isolating cDNAs and genes having similar biological activity.
XX
PS Disclosure; Col 27-28; 54pp; English.
XX
CC This invention describes a novel polynucleotide (I) encoding human ADA2.
CC The products of the invention have cytostatic activity and can be used
CC for gene therapy. (I) is useful for treating cancer; as primers and
CC probes for isolating full length cDNA and genes having similar biological
CC activity. This sequence encodes a polypeptide derived from the human
CC HBGBA67X clone which is an amyloid-like protein found in breast tissue
XX
SQ Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	55.4	Length:	550
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x AAA39470 (1-550)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 6
ABL63343
ID ABL63343 standard; DNA; 550 BP.
XX
AC ABL63343;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:1680.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 1680; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	55.4	Length:	550
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0

```
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     6             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x ABL63343 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 7
ABV73813
ID   ABV73813 standard; cDNA; 550 BP.
XX
AC   ABV73813;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human gamma-synuclein Glu110 variant gene.
XX
KW   Gamma-synuclein; human; single nucleotide polymorphism; SNP;
KW   schizophrenia; neuroleptic; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag= a
FT                   /product= "Gamma-synuclein"
FT                   /transl_except= (pos:213. .215,aa:Glu)
FT   variation       replace(340,T)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200275317-A2.
XX
PD   26-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-EP002872.
XX
PR   15-MAR-2001; 2001US-0276306P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Roberts RC,  Van Oostrum J,  Voshol J,  Tamminga CA;
XX
DR   WPI; 2002-750574/81.
DR   P-PSDB; ABP54932.
XX
PT   Screening for compounds for treating or interfering with the onset of
PT   Schizophrenia Spectrum Disorders, by detecting interactions of candidate
PT   compounds with the gamma-synuclein polypeptide.
XX
PS   Disclosure; Fig 1; 32pp; English.
XX
CC   The present sequence is that of cDNA encoding the Glu-110 isoform of
CC   human gamma-synuclein. The invention relates to an isoform of gamma-
CC   synuclein that is caused by an A/T single nucleotide polymorphism (SNP)
CC   at position 329 of the gamma-synuclein coding sequence. This SNP causes a
CC   glutamic acid to valine change at amino acid position 110 of gamma-
CC   synuclein, and is associated with an increased susceptibility of
CC   individuals to schizophrenia spectrum disorders (SSDs). This is the first
CC   time that a genetic component of SSDs has been identified, and provides a
CC   potential target for diagnosis and treatment of schizophrenia. Gamma-
CC   synuclein polypeptides, especially those containing the E110V mutation,
CC   are used in a claimed method of screening for compounds useful for the
CC   treatment of SSDs, and gamma-synuclein expressing cells are used in a
CC   claimed method of screening for agonist or antagonist compounds. An
CC   oligonucleotide complementary to part of the gamma-synuclein coding
CC   sequence is used for the discrimination of an SNP at position 329 of the
CC   coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
CC   useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR
CC   amplification of a polynucleotide encoding gamma-synuclein and analysis
CC   of the occurrence of the SNP at position 329. A transgenic animal useful
CC   for the study of SSDs is also claimed
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              55.4          Length:         550
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     6             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x ABV73813 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 8
ABV73915
ID   ABV73915 standard; cDNA; 550 BP.
XX
AC   ABV73915;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human gamma-synuclein Val110 variant gene.
XX
KW   Gamma-synuclein; human; single nucleotide polymorphism; SNP;
KW   schizophrenia; neuroleptic; mutant; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag= a
FT                   /product= "Gamma-synuclein"
FT                   /transl_except= (pos:213. .215,aa:Glu)
FT   variation       replace(340,A)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200275317-A2.
XX
PD   26-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-EP002872.
XX
PR   15-MAR-2001; 2001US-0276306P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Roberts RC,  Van Oostrum J,  Voshol J,  Tamminga CA;
XX
DR   WPI; 2002-750574/81.
DR   P-PSDB; ABP54933.
XX
PT   Screening for compounds for treating or interfering with the onset of
PT   Schizophrenia Spectrum Disorders, by detecting interactions of candidate
PT   compounds with the gamma-synuclein polypeptide.
XX
PS   Disclosure; Page; 32pp; English.
XX
CC   The present sequence is that of cDNA encoding the Val-110 isoform of
CC   human gamma-synuclein. The invention relates to an isoform of gamma-
CC   synuclein that is caused by an A/T single nucleotide polymorphism (SNP)
CC   at position 329 of the gamma-synuclein coding sequence. This SNP causes a
CC   glutamic acid to valine change at amino acid position 110 of gamma-
```

CC synuclein, and is associated with an increased susceptibility of
CC individuals to schizophrenia spectrum disorders (SSDs). This is the first
CC time that a genetic component of SSDs has been identified, and provides a
CC potential target for diagnosis and treatment of schizophrenia. Gamma-
CC synuclein polypeptides, especially those containing the E110V mutation,
CC are used in a claimed method of screening for compounds useful for the
CC treatment of SSDs, and gamma-synuclein expressing cells are used in a
CC claimed method of screening for agonist or antagonist compounds. An
CC oligonucleotide complementary to part of the gamma-synuclein coding
CC sequence is used for the discrimination of an SNP at position 329 of the
CC coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
CC useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR
CC amplification of a polynucleotide encoding gamma-synuclein and analysis
CC of the occurrence of the SNP at position 329. A transgenic animal useful
CC for the study of SSDs is also claimed. Note: The present sequence is not
CC shown in the specification but is derived from the gamma-synuclein
CC sequence given in Fig 1 (see ABV73813)
XX
SQ Sequence 550 BP; 131 A; 145 C; 192 G; 82 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	55.4	Length:	550
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x ABV73915 (1-550)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 9
AAD63568
ID AAD63568 standard; cDNA; 550 BP.
XX
AC AAD63568;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human amyloid-like protein cDNA.
XX
KW Human; genetic disease; muscular dystrophy; cystic fibrosis; cytostatic;
KW scientific research; gene therapy; gene; amyloid-like protein; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12. .395
FT /*tag= a
FT /product= "Human amyloid-like protein"
XX
PN US6639052-B1.
XX
PD 28-OCT-2003.
XX
PF 14-OCT-1999; 99US-00417540.
XX
PR 30-AUG-1995; 95US-0002993P.
PR 30-AUG-1996; 96US-00705771.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA;
XX
DR WPI; 2003-842790/78.
DR P-PSDB; ABW02024.
XX
PT New isolated protein and nucleic acid molecules, useful for diagnostic
PT and therapeutic purposes, e.g. for treating genetic diseases such as
PT muscular dystrophy or cystic fibrosis.
XX
PS Example 5; Fig 1; 0pp; English.
XX
CC The invention relates to isolated new isolated protein and nucleic acid
CC molecules useful for diagnostic and therapeutic purposes. The invention
CC is for treating genetic diseases such as muscular dystrophy or cystic
CC fibrosis, and for in vitro purposes related to scientific research,
CC synthesis of DNA and manufacture of DNA vectors. The invention is useful
CC in gene therapy. The present sequence is human amyloid-like protein cDNA
XX
SQ Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	55.4	Length:	550
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x AAD63568 (1-550)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 10
ADG47636
ID ADG47636 standard; cDNA; 550 BP.
XX
AC ADG47636;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human amyloid like protein cDNA.
XX
KW ss; gene; muscular dystrophy; cystic fibrosis; hypertension;
KW angina pectoris; myocardial infarction; ulcer; asthma; allergy;
KW psychosis; depression; migraine; vomiting; benign prostatic hypertrophy;
KW osteoporosis; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12. .395
FT /*tag= a
FT /product= "Amyloid like protein"
XX
PN US2003208043-A1.
XX
PD 06-NOV-2003.
XX
PF 04-JUN-2003; 2003US-00453478.
XX
PR 30-AUG-1995; 95US-0002993P.
PR 30-AUG-1996; 96US-00705771.
PR 14-OCT-1999; 99US-00417540.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Gentz RL, Ji H, Ni J, Hu J;
XX
DR WPI; 2003-864796/80.
DR P-PSDB; ADG47647.
XX
PT New human polypeptides and polynucleotides, useful for diagnosing or
PT treating genetic diseases such as muscular dystrophy or cystic fibrosis,
PT hypertension, asthma, depression or osteoporosis.
XX
PS Claim 18; SEQ ID NO 1; 56pp; English.
XX
CC The invention relates to an isolated human polypeptide. The polypeptides,
CC polynucleotides, agonists or antagonist are useful for diagnosing or

```
CC   treating genetic diseases such as muscular dystrophy or cystic fibrosis,
CC   hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
CC   allergies, psychoses, depression, migraine, vomiting, benign prostatic
CC   hypertrophy or osteoporosis. The polypeptides and polynucleotides are
CC   useful for in vitro purposes related to scientific research, synthesis of
CC   DNA and manufacture of DNA vector. The present sequence represents cDNA
CC   encoding human amyloid like protein.
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              55.4          Length:         550
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
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DB:                     10            Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x ADG47636 (1-550)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
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Db        369 GAGGAGGCCCAGAGTGGGGGAGAC 392

RESULT 11
AAX29997
ID   AAX29997 standard; DNA; 720 BP.
XX
AC   AAX29997;
XX
DT   06-JUL-1999  (first entry)
XX
DE   Human persyn gene.
XX
KW   Human; synuclein; persyn; diagnosis; neurodegenerative disorder; cancer;
KW   breast; skin; intermediate filament damage; ss.
XX
OS   Homo sapiens.
XX
PN   EP908727-A1.
XX
PD   14-APR-1999.
XX
PF   21-SEP-1998;   98EP-00307628.
XX
PR   19-SEP-1997;   97GB-00019879.
XX
PA   (NEUR-) NEUROPA LTD.
PA   (UYSA-) UNIV ST ANDREWS.
XX
DR   WPI; 1999-217169/19.
DR   P-PSDB; AAY07271.
XX
PT   New synuclein protein (persyn) and gene, useful in assays for screening,
PT   diagnosing or monitoring cancer, neurodegenerative disorders or skin
PT   disorders.
XX
PS   Claim 29; Page 16-17; 39pp; English.
XX
CC   This sequence represents the gene encoding a novel human synuclein family
CC   member designated persyn. The sequence is useful for screening,
CC   diagnosing or monitoring cancer (especially breast or skin cancer),
CC   neurodegenerative disorders or skin disorders and for identifying cells
CC   having intermediate filament damage
XX
SQ   Sequence 720 BP; 173 A; 209 C; 215 G; 123 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              73.5          Length:         720
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     2             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x AAX29997 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 12
ABS76519
ID   ABS76519 standard; cDNA; 720 BP.
XX
AC   ABS76519;
XX
DT   11-DEC-2002  (first entry)
XX
DE   cDNA encoding human ovarian cancer marker OV60.
XX
KW   Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW   central nervous system disorder; bacterial meningitis; viral meningitis;
KW   Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW   brain herniation; inflammation; encephalitis; testicular disorder;
KW   nontuberculous granulomatous orchitis; connective tissue disorder;
KW   heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW   histological type; carcinogenic; ovarian cancer marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200271928-A2.
XX
PD   19-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-US007826.
XX
PR   14-MAR-2001; 2001US-0276025P.
PR   14-MAR-2001; 2001US-0276026P.
PR   10-AUG-2001; 2001US-0311732P.
PR   19-SEP-2001; 2001US-0323580P.
PR   26-SEP-2001; 2001US-0324967P.
PR   26-SEP-2001; 2001US-0325102P.
PR   26-SEP-2001; 2001US-0325149P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Monahan JE,  Gannavarapu M,  Hoersch S,  Kamatkar S,  Kovatis SG;
PI   Meyers RE,  Morrisey MP,  Olandt PJ,  Sen A,  Vieby PO,  Mills GB;
PI   Bast RC,  Lu K,  Schmandt RE,  Zhao X,  Glatt K;
XX
DR   WPI; 2002-723277/78.
DR   P-PSDB; ABG96420.
XX
PT   Assessing whether a patient is afflicted with ovarian cancer, useful in
PT   assessing the stage or progression of the disease, comprises comparing
PT   the expression level of a cancer marker in a sample from a patient and
PT   from a non cancer patient.
XX
PS   Disclosure; Page 411; 481pp; English.
XX
CC   The present invention relates to a new method for assessing whether a
CC   patient is afflicted with ovarian cancer. The method involves comparing
CC   the expression level of a marker in a patient sample and the normal level
CC   of expression of the marker in a control non-ovarian cancer sample, where
CC   the marker is selected from 363 cancer markers described in the
CC   specification. The method of the invention is useful in diagnosing or
CC   characterising cancer, in detecting the presence of cancer as early as
CC   possible, and the recurrence of ovarian cancer. The method may also be of
CC   particular use with patients having an enhanced risk of developing
CC   ovarian cancer (e.g. patients having a familial history of ovarian
CC   cancer). The cancer markers may be used in the management and treatment
CC   of e.g. brain and central nervous system disorders (e.g. bacterial and
CC   viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC   disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
CC   inflammations (e.g. bacterial or viral meningitis or encephalitis),
```

```
CC   testicular disorders (e.g. nontuberculous granulomatous orchitis),
CC   connective tissue disorders, or heart disorders (e.g. ischaemic heart
CC   disease or atherosclerosis). The compositions and methods may also be
CC   used in assessing the histological type of neoplasm associated with
CC   ovarian cancer, monitoring the progression of ovarian cancer, determining
CC   whether ovarian cancer has metastasized or is likely to metastasize,
CC   selecting a composition for inhibiting ovarian cancer, assessing the
CC   ovarian carcinogenic potential of a compound, or inhibiting ovarian
CC   cancer or at risk of developing ovarian cancer. The present nucleic acid
CC   sequence encodes one of the ovarian cancer markers described in the
CC   invention
XX
SQ   Sequence 720 BP; 173 A; 209 C; 215 G; 123 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              73.5          Length:         720
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     6             Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x ABS76519 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 13
ADE43864
ID   ADE43864 standard; cDNA; 720 BP.
XX
AC   ADE43864;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human SNCG cDNA, SEQ ID 469.
XX
KW   Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW   Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW   Chromosome 10; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003054143-A2.
XX
PD   03-JUL-2003.
XX
PF   25-OCT-2002; 2002WO-US034679.
XX
PR   25-OCT-2001; 2001US-0339525P.
PR   08-NOV-2001; 2001US-0336929P.
PR   08-NOV-2001; 2001US-0338010P.
PR   09-NOV-2001; 2001US-0338363P.
PR   04-DEC-2001; 2001US-0337052P.
PR   28-MAR-2002; 2002US-0368919P.
XX
PA   (NEUR-) NEUROGENETICS INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Becker KD,  Velicelebi G,  Elliott KJ,  Wang X,  Tanzi RE,  Bertram L;
PI   Saunders AJ,  Mullin KM,  Sampson AJ,  Blacker DL;
XX
DR   WPI; 2003-559131/52.
XX
PT   Determining a predisposition for or the occurrence of neurodegenerative
PT   disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT   the presence or absence of an allelic variant of one or more polymorphic
PT   regions.
XX
PS   Claim 84; Page 740; 848pp; English.
XX
CC   The present invention relates to a method (M1) for determining a
CC   predisposition for or the occurrence of neurodegenerative disease in a
CC   subject. The method comprises detecting in a target nucleic acid obtained
CC   from the subject the presence or absence of an allelic variant of one or
CC   more polymorphic regions of one or more genes selected from uPA
CC   (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC   degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
CC   lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC   presence of at least one of the allelic variant of one or more
CC   polymorphic regions is indicative of a predisposition for or the
CC   occurrence of neurodegenerative disease. The genes are all located on
CC   chromosome 10. M1 is useful for determining a predisposition for or the
CC   occurrence of, and for treating neurodegenerative disease, particularly
CC   Alzheimer's disease.
XX
SQ   Sequence 720 BP; 172 A; 205 C; 212 G; 120 T; 0 U; 11 Other;

Alignment Scores:
Pred. No.:              73.5          Length:         720
Score:                  41.00         Matches:        8
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     10            Gaps:           0

US-09-017-715A-2_COPY_120_127 (1-8) x ADE43864 (1-720)

Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429

RESULT 14
ADH54342
ID   ADH54342 standard; cDNA; 720 BP.
XX
AC   ADH54342;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human SNCG gene cDNA sequence SeqID469.
XX
KW   human; neurodegenerative disease; urokinase plasminogen activator; uPA;
KW   gamma-synuclein; SNCG; insulin degrading enzyme; IDE;
KW   kinesin-like protein 1; KNSL1; lysosomal acid lipase; LIPA;
KW   tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; ss.
XX
OS   Homo sapiens.
XX
PN   US2003224380-A1.
XX
PD   04-DEC-2003.
XX
PF   25-OCT-2002; 2002US-00282174.
XX
PR   25-OCT-2001; 2001US-0339525P.
PR   25-OCT-2001; 2001US-0348065P.
PR   02-NOV-2001; 2001US-0336983P.
PR   08-NOV-2001; 2001US-0336929P.
PR   08-NOV-2001; 2001US-0338010P.
PR   09-NOV-2001; 2001US-0338363P.
PR   04-DEC-2001; 2001US-0337052P.
PR   28-MAR-2002; 2002US-0368919P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Becker KD,  Velicelebi G,  Ellliott KJ,  Wang X,  Tanzi RE;
PI   Bertram L,  Saunders AJ,  Mullin KM,  Sampson AJ;
XX
DR   WPI; 2004-060538/06.
XX
PT   Determining a predisposition for or the occurrence of neurodegenerative
PT   disease, particularly Alzheimer's disease, comprises determining the
PT   presence of a polymorphism in the uPA, SNCG, IDE, KNSL1, LIPA or TNFRSF6
PT   gene.
```

XX
PS Claim 84; SEQ ID NO 469; 205pp; English.
XX
CC This invention relates to a novel method of determining a predisposition
CC for or the occurrence of neurodegenerative disease comprising detecting
CC in a target nucleic acid obtained from the subject the presence of an
CC allelic variant of polymorphic regions of human genes selected from
CC urokinase plasminogen activator (uPA), gamma-synuclein (SNCG), insulin
CC degrading enzyme (IDE), kinesin-like protein 1 (KNSL1), lysosomal acid
CC lipase (LIPA) and tumour necrosis factor receptor SF6 (TNFRSF6). The
CC method is useful in determining the presence or predisposition to a
CC neurodegenerative disease, particularly Alzheimer's disease. The present
CC sequence is the cDNA sequence of the human SNCG gene which is related to
CC the invention.
XX
SQ Sequence 720 BP; 172 A; 205 C; 212 G; 120 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.:	73.5	Length:	720
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-017-715A-2_COPY_120_127 (1-8) x ADH54342 (1-720)

```
Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        406 GAGGAGGCCCAGAGTGGGGGAGAC 429
```

RESULT 15
AAI93778
ID AAI93778 standard; cDNA; 783 BP.
XX
AC AAI93778;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 13838.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR P-PSDB; AAO13847.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 1; SEQ ID NO 13838; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 783 BP; 187 A; 232 C; 237 G; 127 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	80.3	Length:	783
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-017-715A-2_COPY_120_127 (1-8) x AAI93778 (1-783)

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Qy          1 GluGluAlaGlnSerGlyGlyAsp 8
              ||||||||||||||||||||||||
Db        471 GAGGAGGCCCAGAGTGGGGGAGAC 494
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GenCore version 5.1.6

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	610	100.0	550	4	US-09-417-540-1	Sequence 1, Appli
3	602	98.7	702	4	US-09-949-016-1915	Sequence 1915, Ap
4	595	97.5	720	4	US-09-949-016-442	Sequence 442, App
5	468.5	76.8	786	5	PCT-US95-08295-1	Sequence 1, Appli
6	307.5	50.4	1543	4	US-09-949-016-58	Sequence 58, Appl
7	307.5	50.4	1543	4	US-09-949-016-3084	Sequence 3084, Ap
8	307.5	50.4	1543	4	US-09-949-016-3085	Sequence 3085, Ap
9	307.5	50.4	1560	5	PCT-US94-09789-1	Sequence 1, Appli
10	303.5	49.8	1096	4	US-09-949-016-3086	Sequence 3086, Ap
11	303.5	49.8	1096	4	US-09-949-016-3087	Sequence 3087, Ap
12	284.5	46.6	703	4	US-09-949-016-2926	Sequence 2926, Ap
13	282	46.2	313	4	US-09-513-999C-2232	Sequence 2232, Ap
14	201.5	33.0	8607	4	US-09-949-016-13657	Sequence 13657, A
15	201.5	33.0	8608	4	US-09-949-016-12184	Sequence 12184, A
16	187	30.7	419	4	US-09-621-976-609	Sequence 609, App
17	184	30.2	409	4	US-09-513-999C-2347	Sequence 2347, Ap
18	171	28.0	8281	4	US-09-949-016-14668	Sequence 14668, A
19	155	25.4	113876	4	US-09-949-016-14828	Sequence 14828, A
20	155	25.4	113876	4	US-09-949-016-14829	Sequence 14829, A
21	155	25.4	115508	4	US-09-949-016-11800	Sequence 11800, A
22	155	25.4	115508	4	US-09-949-016-14826	Sequence 14826, A
23	155	25.4	115508	4	US-09-949-016-14827	Sequence 14827, A
c 24	113	18.5	601	4	US-09-949-016-18715	Sequence 18715, A
c 25	113	18.5	601	4	US-09-949-016-111590	Sequence 111590,
c 26	113	18.5	601	4	US-09-949-016-111738	Sequence 111738,
c 27	113	18.5	601	4	US-09-949-016-111884	Sequence 111884,
c 28	113	18.5	601	4	US-09-949-016-112029	Sequence 112029,
29	98	16.1	387	5	PCT-US96-05320A-1342	Sequence 1342, Ap
c 30	98	16.1	845	2	US-08-743-637B-25	Sequence 25, Appl
c 31	98	16.1	845	3	US-08-526-840B-25	Sequence 25, Appl
32	98	16.1	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 33	98	16.1	1830121	4	US-09-557-884-1	Sequence 1, Appli
34	98	16.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c 35	98	16.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli
36	95	15.6	729	4	US-09-543-681A-1761	Sequence 1761, Ap
37	94	15.4	1695	2	US-08-216-894-1	Sequence 1, Appli
38	94	15.4	1695	3	US-09-115-746-1	Sequence 1, Appli
39	94	15.4	1932	2	US-08-216-894-7	Sequence 7, Appli
40	94	15.4	1932	3	US-09-115-746-7	Sequence 7, Appli
41	94	15.4	5361	3	US-08-973-462-2	Sequence 2, Appli
42	94	15.4	6152	3	US-08-973-462-1	Sequence 1, Appli
43	93	15.2	6717	4	US-09-107-433-1903	Sequence 1903, Ap
44	92.5	15.2	2787	4	US-09-134-000C-3185	Sequence 3185, Ap
c 45	92	15.1	3506	4	US-09-710-279-3423	Sequence 3423, Ap

ALIGNMENTS

RESULT 1
US-08-705-771-1
; Sequence 1, Application US/08705771
; Patent No. 6054289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,771
; FILING DATE: August 30, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```
;      LENGTH:  550 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-705-771-1

Alignment Scores:
Pred. No.:              2.15e-69        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-09-017-715A-2 (1-127) x US-08-705-771-1 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 2
US-09-417-540-1
; Sequence 1, Application US/09417540
; Patent No. 6639052
;   GENERAL INFORMATION:
;        APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                   Jian Ni and Jing-Shan Hu
;        TITLE OF INVENTION: Human Genes, Sequences and
;                            Expression Products
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                        CECCHI, STEWART & OLSTEIN
;             STREET: 6 BECKER FARM ROAD
;             CITY: ROSELAND
;             STATE: NEW JERSEY
;             COUNTRY: USA
;             ZIP: 07068
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 INCH DISKETTE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: MS-DOS
;             SOFTWARE: WORD PERFECT 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/417,540
;             FILING DATE: 14-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/705,771
;             FILING DATE: August 30, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MULLINS, J.G.
;             REGISTRATION NUMBER: 33,073
;             REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 973-994-1700
;             TELEFAX: 973-994-1744
;    INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 550 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-417-540-1

Alignment Scores:
Pred. No.:              2.15e-69        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2 (1-127) x US-09-417-540-1 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 3
US-09-949-016-1915
; Sequence 1915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
```

```
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1915
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1915

Alignment Scores:
Pred. No.:              3.29e-68        Length:         702
Score:                  602.00          Matches:        125
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  98.43%          Mismatches:     0
Query Match:            98.69%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2 (1-127) x US-09-949-016-1915 (1-702)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         48 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 107

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 167

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 227

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        228 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 287

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 347

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 407

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        408 GAGGCCCAGAGTGGGGGAGAC 428

RESULT 4
US-09-949-016-442
; Sequence 442, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 442
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-442

Alignment Scores:
Pred. No.:              2.72e-67        Length:         720
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     4               Gaps:           0

US-09-017-715A-2 (1-127) x US-09-949-016-442 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         49 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 5
PCT-US95-08295-1
; Sequence 1, Application PC/TUS9508295
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  BREAST SPECIFIC GENES AND PROTEINS
;    NUMBER OF SEQUENCES:  30
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08295
;      FILING DATE:  30-JUN-1995
;      CLASSIFICATION:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  786 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-08295-1

Alignment Scores:
Pred. No.:              5.95e-51        Length:         786
Score:                  468.50          Matches:        111
Percent Similarity:     86.15%          Conservative:   1
Best Local Similarity:  85.38%          Mismatches:     15
Query Match:            76.80%          Indels:         4
DB:                     5               Gaps:           1

US-09-017-715A-2 (1-127) x PCT-US95-08295-1 (1-786)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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                ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         95 ATGGATGTYTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 154

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 214

Qy         41 GlyAlaLysThrLysGluAsn---Val-ValGlnSerValThrSerValAlaGluLysTh 59
                ||||||||||||||||||    ||| ||||||||||||||||||||||||||||||||
Db        215 GGAGCCAAGACCAAGGAGAATGTTGTATGTACAGAGCGTGACCTCAGTGGCCGAGAAGAC 274

Qy         59 rLysGluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaTh 79
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CAAGGAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTKTGGCCAC 334

Qy         79 rLysThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAs 99
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 CAAGACCGTKGAGGAGGCGGAGAACATCGCGGTCAMCTCCGGGKTGKTGCGCAAGGAGGA 394

Qy         99 pLeuArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGlu-LysGluGluValA 119
                |    ||||||      ||||||||||||||||||||||||||   |||              |
Db        395 YTTKAGGCCATY-TKCCCCCAACAGGAGGGTGAGGCATCMARAGARARGAKWGSAAGWGG 453

Qy        119 laGluGluAlaGlnSerGlyGlyAsp 127
                ||      ||||||||||||||
Db        454 CMRAKKRGGMSCAGAGTGGGGGAGAC 479

RESULT 6
US-09-949-016-58
; Sequence 58, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
;   LENGTH: 1543
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-58

Alignment Scores:
Pred. No.:              8.5e-30       Length:          1543
Score:                  307.50        Matches:         68
Percent Similarity:     70.91%        Conservative:    10
Best Local Similarity:  61.82%        Mismatches:      29
Query Match:            50.41%        Indels:          3
DB:                     4             Gaps:            1

US-09-017-715A-2 (1-127) x US-09-949-016-58 (1-1543)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
                ||||||||||||   ||||||   |||   ||||||:::|||||||||   |||   |||
Db         47 ATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 106

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
                |||||||||||||||||   |||||||||   ||||||||||||||||||:::||||||
Db        107 AAAACCAAACAGGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTTCTCTATGTA 166

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
                |||:::||||||||||||   ||||||      |||   :::||||||||||||||||||
Db        167 GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAACAGTGGCTGAGAAGACCAAA 226

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
                ||||||          |||      |||||||||:::   |||      ||||||   |||
Db        227 GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG 286

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
                |||||||||   |||   :::||||||      :::|||   |||:::|||:::   |||
Db        287 ACAGTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG 346

Qy        101 ---------ArgProSerAlaProGlnGln 107
                         |||||||||:::
Db        347 GGCAAGAATGAAGAAGGAGCCCCACAGGAA 376

RESULT 7
US-09-949-016-3084
; Sequence 3084, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3084
;   LENGTH: 1543
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3084

Alignment Scores:
Pred. No.:              8.5e-30       Length:          1543
Score:                  307.50        Matches:         68
Percent Similarity:     70.91%        Conservative:    10
Best Local Similarity:  61.82%        Mismatches:      29
Query Match:            50.41%        Indels:          3
DB:                     4             Gaps:            1

US-09-017-715A-2 (1-127) x US-09-949-016-3084 (1-1543)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
                ||||||||||||   ||||||   |||   ||||||:::|||||||||   |||   |||
Db         47 ATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 106

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
                |||||||||||||||||   |||||||||   ||||||||||||||||||:::||||||
Db        107 AAAACCAAACAGGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTTCTCTATGTA 166

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
                |||:::||||||||||||   ||||||      |||   :::||||||||||||||||||
Db        167 GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAACAGTGGCTGAGAAGACCAAA 226

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
                ||||||          |||      |||||||||:::   |||      ||||||   |||
Db        227 GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG 286

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
                |||||||||   |||   :::||||||      :::|||   |||:::|||:::   |||
Db        287 ACAGTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG 346

Qy        101 ---------ArgProSerAlaProGlnGln 107
                         |||||||||:::
Db        347 GGCAAGAATGAAGAAGGAGCCCCACAGGAA 376

RESULT 8
```

```
US-09-949-016-3085
; Sequence 3085, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3085
;   LENGTH: 1543
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3085

Alignment Scores:
Pred. No.:              8.5e-30       Length:          1543
Score:                  307.50        Matches:         68
Percent Similarity:     70.91%        Conservative:    10
Best Local Similarity:  61.82%        Mismatches:      29
Query Match:            50.41%        Indels:          3
DB:                     4             Gaps:            1

US-09-017-715A-2 (1-127) x US-09-949-016-3085 (1-1543)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||  ||||||  |||  ||||||:::|||||||||  |||  |||
Db         47 ATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 106

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||  |||||||||  ||||||||||||||||||:::||||||
Db        107 AAAACCAAACAGGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTTCTCTATGTA 166

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||||||||  ||||||      |||   :::|||||||||||||||||||
Db        167 GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAACAGTGGCTGAGAAGACCAAA 226

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||      |||      |||||||||:::   |||      ||||||  |||
Db        227 GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG 286

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              |||||||||   |||   :::|||||||      :::|||   |||:::|||:::   |||
Db        287 ACAGTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG 346

Qy        101 ---------ArgProSerAlaProGlnGln 107
                        |||||||||:::
Db        347 GGCAAGAATGAAGAAGGAGCCCCACAGGAA 376

RESULT 9
PCT-US94-09789-1
; Sequence 1, Application PC/TUS9409789
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    TITLE OF INVENTION:  NOVEL COMPONENT OF AMYLOID IN
;    TITLE OF INVENTION:  ALZHEIMER'S DISEASE AND METHODS FOR USE OF SAME
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East - Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09789
;      FILING DATE:  29-AUG-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  FD-3520
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  cDNA for NACP
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  1..1560
PCT-US94-09789-1

Alignment Scores:
Pred. No.:              8.64e-30      Length:          1560
Score:                  307.50        Matches:         68
Percent Similarity:     70.91%        Conservative:    10
Best Local Similarity:  61.82%        Mismatches:      29
Query Match:            50.41%        Indels:          3
DB:                     5             Gaps:            1

US-09-017-715A-2 (1-127) x PCT-US94-09789-1 (1-1560)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||  ||||||  |||  ||||||:::|||||||||  |||  |||
Db         53 ATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 112

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||  |||||||||  ||||||||||||||||||:::||||||
Db        113 AAAACCAAACAGGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTTCTCTATGTA 172

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||||||||  ||||||      |||   :::|||||||||||||||||||
Db        173 GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAACAGTGGCTGAGAAGACCAAA 232

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||      |||      |||||||||:::   |||      ||||||  |||
Db        233 GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG 292

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              |||||||||   |||   :::|||||||      :::|||   |||:::|||:::   |||
Db        293 ACAGTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG 352

Qy        101 ---------ArgProSerAlaProGlnGln 107
                        |||||||||:::
Db        353 GGCAAGAATGAAGAAGGAGCCCCACAGGAA 382

RESULT 10
US-09-949-016-3086
; Sequence 3086, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
```

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;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3086
;   LENGTH: 1096
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3086

Alignment Scores:
Pred. No.:              1.68e-29        Length:         1096
Score:                  303.50          Matches:        69
Percent Similarity:     68.10%          Conservative:   10
Best Local Similarity:  59.48%          Mismatches:     32
Query Match:            49.75%          Indels:         5
DB:                     4               Gaps:           1

US-09-017-715A-2 (1-127) x US-09-949-016-3086 (1-1096)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||   ||||||   |||   ||||||:::|||||||||   |||   |||
Db         14 ATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 73

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||   |||||||||   |||||||||||||||||||:::||||||
Db         74 AAAACCAAACAGGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTTCTCTATGTA 133

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||||||||   ||||||      |||   :::||||||||||||||||||
Db        134 GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAACAGTGGCTGAGAAGACCAAA 193

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||          |||      |||||||||:::   |||      ||||||   |||
Db        194 GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG 253

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              |||||||||   |||   :::||||||      :::|||   |||:::|||:::   |||
Db        254 ACAGTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG 313

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGlu 116
                          :::||||||            |||   |||
Db        314 --------------GGCAAGGAAGGGTATCAAGACTACGAACCTGAA 346

RESULT 11
US-09-949-016-3087
; Sequence 3087, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3087
;   LENGTH: 1096
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3087

Alignment Scores:
Pred. No.:              1.68e-29        Length:         1096
Score:                  303.50          Matches:        69
Percent Similarity:     68.10%          Conservative:   10
Best Local Similarity:  59.48%          Mismatches:     32
Query Match:            49.75%          Indels:         5
DB:                     4               Gaps:           1

US-09-017-715A-2 (1-127) x US-09-949-016-3087 (1-1096)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||   ||||||   |||   ||||||:::|||||||||   |||   |||
Db         14 ATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAG 73

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||   |||||||||   |||||||||||||||||||:::||||||
Db         74 AAAACCAAACAGGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTTCTCTATGTA 133

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||||||||   ||||||      |||   :::||||||||||||||||||
Db        134 GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAACAGTGGCTGAGAAGACCAAA 193

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||          |||      |||||||||:::   |||      ||||||   |||
Db        194 GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG 253

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              |||||||||   |||   :::||||||      :::|||   |||:::|||:::   |||
Db        254 ACAGTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG 313

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGlu 116
                          :::||||||            |||   |||
Db        314 --------------GGCAAGGAAGGGTATCAAGACTACGAACCTGAA 346

RESULT 12
US-09-949-016-2926
; Sequence 2926, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2926
;   LENGTH: 703
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2926

Alignment Scores:
Pred. No.:              2.45e-27        Length:         703
Score:                  284.50          Matches:        61
Percent Similarity:     73.74%          Conservative:   12
Best Local Similarity:  61.62%          Mismatches:     15
Query Match:            46.64%          Indels:         11
DB:                     4               Gaps:           1

US-09-017-715A-2 (1-127) x US-09-949-016-2926 (1-703)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||   ||||||   |||:::||||||:::|||||||||   |||   |||
```

```
Db        418 ATGGACGTGTTCATGAAGGGCCTGTCCATGGCCAAGGAGGGCGTTGTGGCAGCCGCGGAG 477

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        478 AAAACCAAGCAGGGGGTCACCGAGGCGGCGGAGAAGACCAAGGAGGGCGTCCTCTACGTC 537

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              |||:::||||||:::|||   |||||||||   |||   ||||||||||||||||||||
Db        538 GGAAGCAAGACCCGAGAAGGTGTGGTACAAGGTGTGGCTTCAGTGGCTGAAAAAACCAAG 597

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              |||||||||:::   :::     ||||||  |||
Db        598 GAACAGGCCTCACATCTGGGAGGAGCTGTGTTCTCTGGG---------------------- 636

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAsp 99
                        |||   |||||||||      :::|||:::|||:::::::|||:::
Db        637 ------------GCAGGGAACATCGCAGCAGCCACAGGACTGGTGAAGAGGGAGGAA 681

RESULT 13
US-09-513-999C-2232
; Sequence 2232, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 2232
;   LENGTH: 313
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 136..312
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 117
;   OTHER INFORMATION: m=a or c
US-09-513-999C-2232

Alignment Scores:
Pred. No.:              1.56e-27      Length:          313
Score:                  282.00        Matches:         58
Percent Similarity:     100.00%       Conservative:    1
Best Local Similarity:  98.31%        Mismatches:      0
Query Match:            46.23%        Indels:          0
DB:                     4             Gaps:            0

US-09-017-715A-2 (1-127) x US-09-513-999C-2232 (1-313)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        136 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 195

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 255

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThr 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACC 312

RESULT 14
US-09-949-016-13657
; Sequence 13657, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13657
;   LENGTH: 8607
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(8607)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13657

Alignment Scores:
Pred. No.:              4.69e-15      Length:          8607
Score:                  201.50        Matches:         97
Percent Similarity:     20.66%        Conservative:    3
Best Local Similarity:  20.04%        Mismatches:      3
Query Match:            33.03%        Indels:          383
DB:                     4             Gaps:            2

US-09-017-715A-2 (1-127) x US-09-949-016-13657 (1-8607)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       2048 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 2107

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2108 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 2167

Qy         40 ---------------------------------------------------------- 40

Db       2168 GGTAAGTGGGGCATGGCAGGGTGGGACAGTGTGGTGGCCAAAGGGTGAGTGCCCAGTTAC 2227

Qy         40 ---------------------------------------------------------- 40

Db       2228 CTTCGCCAGACCTTACTCCCCAGCCCCAGGGAGGCATTTTGGGAGGGGGCGAGGCCCTGG 2287

Qy         40 ---------------------------------------------------------- 40

Db       2288 CTATCAAGGTGGGGTCTCCAGACCCTGGAGCACCCACAATGCCCTGTGCACACCTATGTG 2347

Qy         40 ---------------------------------------------------------- 40

Db       2348 TGTTTGTCTTTGGCCTCCTCGGGGCCTCTGGGTGTCAGAGACCGCAGACAGGGCTGGCTA 2407

Qy         40 ---------------------------------------------------------- 40

Db       2408 CCTGTCTGTGCACGCACACACACATTCCCAAGCATACCAGCCTCCCCTGAGCCTGGAGCC 2467

Qy         40 ---------------------------------------------------------- 40

Db       2468 CCTGAAGCCATGAGCAGCCTGTGCTCAGGTGGCCCCCACCCTCTCCACACGGGAGCGGCT 2527

Qy         40 ---------------------------------------------------------- 40

Db       2528 ACAGCCAGGTCACGGATCCCCTCCCTCCCCAGAGAGAAGGGGCAGGCTGGGGGATGAAAC 2587

Qy         40 ---------------------------------------------------------- 40
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Db       2588 CTAGGCTCAGTGTTCCCTCCCCCGCATCCTCTCCTGGCACTCTCCAGAGGAGGAAGGGGA 2647

Qy         40 ------------------------------------------------------------ 40

Db       2648 GGTCAAGCCAATGACTCAGCTCTGGCCCATCCTGTCCTGTTGCTGCTTCTGAGGCCCGGC 2707

Qy         40 ------------------------------------------------------------ 40

Db       2708 CACACCCGGGCAGGGGCTGGACCCTGGGTCTAGCCAGTGTCCCTACCTCAGGCCTGCTCT 2767

Qy         40 ------------------------------------------------------------ 40

Db       2768 CTCTTGTCCCCCACATTCTGTCCTGTCCCCTTCCCATCCATCCACTTCTTCCAGACACAG 2827

Qy         40 ------------------------------------------------------------ 40

Db       2828 CAGGAAGAGGCCCTCTGAAGGGGCCGCCGGCCCCCAGACACCATCCTTACCCCCCCACCG 2887

Qy         40 ------------------------------------------------------------ 40

Db       2888 ACCCCACAGTTTGTCCAGCTGTTCTGTTGTGTTTGTCCTGACCGCCCCCAACACCTCGAG 2947

Qy         41 ---------------------------------GlyAlaLysThrLysGluAsnValVa 49
                                               ||||||||||||||||||||||||
Db       2948 GGAGGTCTGGGCTGACAGCTCCATTTCCTCCCCAGGAGCCAAGACCAAGGAGAATGTTGT 3007

Qy         49 lGlnSerValThrSer---------------------------------------------- 54
              ||||||||||||
Db       3008 ACAGAGCGTGACCTC-AGGTGAGAAGCCCCAGGGCCAGGGGACACATGGGGGATAGGACC 3066

Qy         54 ------------------------------------------------------------ 54

Db       3067 CCTGGGGCTCCTGCATCCTAGTGCTGGGGCTCAAACCTAGAGTCCTGCCTTACCCCCAAC 3126

Qy         54 ------------------------------------------------------------ 54

Db       3127 TGGGGTCCCAAGCCCTACAGACCCCTGCAGACCATGAGGCTAAACTAGGGTGGGCGTCTC 3186

Qy         54 ------------------------------------------------------------ 54

Db       3187 CTTACCCCCACCAGCATCAGAGGTGCCCTGGAGTCAGAGGGAGCAGGGGAGGGTCCCAGC 3246

Qy         54 ------------------------------------------------------------ 54

Db       3247 AGGGCCAGGGCTCTGAGCTCCTGGGAAGGGGCTGCGAGCCTGACTCCAGCAGGCCTGCCT 3306

Qy         55 ---------------------------------------------ValAlaGluLysThrLy 60
                                                           ||||||||||||||||||
Db       3307 TGGGGCTGGGGCTGGGGTGGAGGCCAGCCAGTGTCCTCCCATAGTGGCCGAGAAGACCAA 3366

Qy         60 sGluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLy 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       3367 GGAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAA 3426

Qy         80 sThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db       3427 GACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGT-GAGCC 3485

Qy        100 uArgProSer 103
              |||||||||
Db       3486 CCGGCCCTCA 3495

RESULT 15
US-09-949-016-12184
; Sequence 12184, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12184
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(8608)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12184

Alignment Scores:
Pred. No.:                4.69e-15        Length:          8608
Score:                    201.50          Matches:         97
Percent Similarity:       20.66%          Conservative:    3
Best Local Similarity:    20.04%          Mismatches:      3
Query Match:              33.03%          Indels:          383
DB:                       4               Gaps:            2

US-09-017-715A-2 (1-127) x US-09-949-016-12184 (1-8608)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       2048 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 2107

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2108 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 2167

Qy         40 ------------------------------------------------------------ 40

Db       2168 GGTAAGTGGGGCATGGCAGGGTGGGACAGTGTGGTGGCCAAAGGGTGAGTGCCCAGTTAC 2227

Qy         40 ------------------------------------------------------------ 40

Db       2228 CTTCGCCAGACCTTACTCCCCAGCCCCAGGGAGGCATTTTGGGAGGGGGCGAGGCCCTGG 2287

Qy         40 ------------------------------------------------------------ 40

Db       2288 CTATCAAGGTGGGGTCTCCAGACCCTGGAGCACCCACAATGCCCTGTGCACACCTATGTG 2347

Qy         40 ------------------------------------------------------------ 40

Db       2348 TGTTTGTCTTTGGCCTCCTCGGGGCCTCTGGGTGTCAGAGACCGCAGACAGGGCTGGCTA 2407

Qy         40 ------------------------------------------------------------ 40

Db       2408 CCTGTCTGTGCACGCACACACACATTCCCAAGCATACCAGCCTCCCCTGAGCCTGGAGCC 2467

Qy         40 ------------------------------------------------------------ 40

Db       2468 CCTGAAGCCATGAGCAGCCTGTGCTCAGGTGGCCCCCACCCTCTCCACACGGGAGCGGCT 2527

Qy         40 ------------------------------------------------------------ 40

Db       2528 ACAGCCAGGTCACGGATCCCCTCCCTCCCCAGAGAGAAGGGGCAGGCTGGGGGATGAAAC 2587

Qy         40 ------------------------------------------------------------ 40

Db       2588 CTAGGCTCAGTGTTCCCTCCCCCGCATCCTCTCCTGGCACTCTCCAGAGGAGGAAGGGGA 2647

Qy         40 ------------------------------------------------------------ 40

Db       2648 GGTCAAGCCAATGACTCAGCTCTGGCCCATCCTGTCCTGTTGCTGCTTCTGAGGCCCGGC 2707
```

```
Qy         40 ------------------------------------------------------------ 40

Db       2708 CACACCCGGGCAGGGGCTGGACCCTGGGTCTAGCCAGTGTCCCTACCTCAGGCCTGCTCT 2767

Qy         40 ------------------------------------------------------------ 40

Db       2768 CTCTTGTCCCCCACATTCTGTCCTGTCCCCTTCCCATCCATCCACTTCTTCCAGACACAG 2827

Qy         40 ------------------------------------------------------------ 40

Db       2828 CAGGAAGAGGCCCTCTGAAGGGGCCGCCGGCCCCCAGACACCATCCTTACCCCCCCACCG 2887

Qy         40 ------------------------------------------------------------ 40

Db       2888 ACCCCACAGTTTGTCCAGCTGTTCTGTTGTGTTTGTCCTGACCGCCCCCAACACCTCGAG 2947

Qy         41 ----------------------------------GlyAlaLysThrLysGluAsnValVa 49
                                                 ||||||||||||||||||||||||
Db       2948 GGAGGTCTGGGCTGACAGCTCCATTTCCTCCCCAGGAGCCAAGACCAAGGAGAATGTTGT 3007

Qy         49 lGlnSerValThrSer---------------------------------------------- 54
              |||||||||||||
Db       3008 ACAGAGCGTGACCTC-AGGTGAGAAGCCCCAGGGCCAGGGGACACATGGGGGATAGGACC 3066

Qy         54 ------------------------------------------------------------ 54

Db       3067 CCTGGGGCTCCTGCATCCTAGTGCTGGGGCTCAAACCTAGAGTCCTGCCTTACCCCCAAC 3126

Qy         54 ------------------------------------------------------------ 54

Db       3127 TGGGGTCCCAAGCCCTACAGACCCCTGCAGACCATGAGGCTAAACTAGGGTGGGCGTCTC 3186

Qy         54 ------------------------------------------------------------ 54

Db       3187 CTTACCCCCACCAGCATCAGAGGTGCCCTGGAGTCAGAGGGAGCAGGGGAGGGTCCCAGC 3246

Qy         54 ------------------------------------------------------------ 54

Db       3247 AGGGCCAGGGCTCTGAGCTCCTGGGAAGGGGCTGCGAGCCTGACTCCAGCAGGCCTGCCT 3306

Qy         55 ------------------------------------------ValAlaGluLysThrLy 60
                                                        ||||||||||||||||
Db       3307 TGGGGCTGGGGCTGGGGTGGAGGCCAGCCAGTGTCCTCCCATAGTGGCCGAGAAGACCAA 3366

Qy         60 sGluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLy 80
              |||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       3367 GGAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAA 3426

Qy         80 sThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLe 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db       3427 GACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGT-GAGCC 3485

Qy        100 uArgProSer 103
              |||||||||
Db       3486 CCGGCCCTCA 3495
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Search completed: May 4, 2005, 09:32:13
Job time : 305.06 secs

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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2005, 09:07:52 ; Search time 928.208 Seconds
(without alignments)
809.955 Million cell updates/sec

Title: US-09-017-715A-2
Perfect score: 610
Sequence: 1 MDVFKKGFSIAKKGVVGAVE.....EGEASKEKEEVAEEAQSGGD 127

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100743_25600/app_query.fasta_1.661
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_@CGN_1_1_703_@runat_04052005_100743_25600 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	610	100.0	550	2	AAV42669	Aav42669 Human bre
2	610	100.0	550	3	AAA39470	Aaa39470 Human HBG
3	610	100.0	550	6	ABL63343	Abl63343 Breast ca
4	610	100.0	550	6	ABV73813	Abv73813 Human gam
5	610	100.0	550	10	AAD63568	Aad63568 Human amy
6	610	100.0	550	10	ADG47636	Adg47636 Human amy
7	603	98.9	550	6	ABV73915	Abv73915 Human gam
8	602	98.7	783	4	AAI93778	Aai93778 Human pol
9	602	98.7	796	3	AAF21784	Aaf21784 Human bre
10	595	97.5	488	12	ADM66887	Adm66887 Human hom
11	595	97.5	720	2	AAX29997	Aax29997 Human per
12	595	97.5	720	6	ABS76519	Abs76519 cDNA enco
13	592	97.0	720	10	ADE43864	Ade43864 Human SNC
14	592	97.0	720	12	ADH54342	Adh54342 Human SNC
15	538	88.2	479	9	ACH15493	Ach15493 Human adu
16	497	81.5	727	2	AAX29998	Aax29998 Mouse per
17	497	81.5	727	12	ADM66886	Adm66886 Murine ad
18	491.5	80.6	787	2	AAT51183	Aat51183 Human bre
19	468.5	76.8	786	9	ADA57841	Ada57841 Human cDN
20	464.5	76.1	990	13	ADR98806	Adr98806 Lung spec
21	328	53.8	210	4	AAD14356	Aad14356 Human gam
22	316	51.8	1018	10	ADB52898	Adb52898 Primary r
23	316	51.8	1018	10	ABT42008	Abt42008 Toxicity
24	316	51.8	1018	12	ADP71875	Adp71875 Renal tox
25	307.5	50.4	423	4	AAD14354	Aad14354 Human alp
26	307.5	50.4	423	6	AAD44409	Aad44409 Human alp
27	307.5	50.4	1105	8	AAL60583	Aal60583 GST-human
28	307.5	50.4	1466	6	ABZ35251	Abz35251 Human gen
29	307.5	50.4	1543	12	ADO24508	Ado24508 Human PRO
30	307.5	50.4	1543	12	ADP44624	Adp44624 Human alp
31	307.5	50.4	1560	2	AAQ83201	Aaq83201 Precursor
32	304.5	49.9	755	12	ADM86918	Adm86918 Human pro
33	304	49.8	441	8	ABX47454	Abx47454 Bovine ES
34	304	49.8	453	8	ABX39864	Abx39864 Bovine ES
35	303.5	49.8	1096	10	ADB37445	Adb37445 Human can
36	303.5	49.8	1096	12	ADP44633	Adp44633 Human alp
37	303.5	49.8	1228	4	AAS02053	Aas02053 DNA encod
38	282	46.2	313	3	AAC02234	Aac02234 Human sec
39	253	41.5	249	4	AAD14355	Aad14355 Human bet
40	243	39.8	424	8	ABX36813	Abx36813 Bovine ES
41	233	38.2	473	9	ACH14620	Ach14620 Human adu
42	212.5	34.8	677	2	AAX04876	Aax04876 Human gam
43	205	33.6	456	9	ACH39765	Ach39765 Human foe
44	202	33.1	393	8	ABX38204	Abx38204 Bovine ES
45	201.5	33.0	4606	6	ABT10161	Abt10161 Human bre

ALIGNMENTS

RESULT 1
AAV42669
ID AAV42669 standard; cDNA; 550 BP.
XX
AC AAV42669;
XX
DT 09-NOV-1998 (first entry)
XX
DE Human breast cancer specific gene 1 (BCSG1) cDNA.
XX
KW Breast cancer specific gene 1; BCGS1; human; metastasis; diagnosis;
KW therapy; genetic marker; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12. .395
FT /*tag= a
XX
PN WO9833915-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US001804.
XX
PR 03-FEB-1997; 97US-0037080P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

```
PI   Ji H,  Rosen CA;
XX
DR   WPI; 1998-446811/38.
DR   P-PSDB; AAW63123.
XX
PT   New isolated human breast cancer specific gene - used to develop products
PT   for the diagnosis, clinical management and treatment of breast cancer and
PT   metastases.
XX
PS   Claim 4; Fig 1; 73pp; English.
XX
CC   This cDNA clone corresponds to the transcript of the newly identified
CC   human breast cancer specific gene 1 (BCSG1), and includes an open reading
CC   frame for a 14.2 kDa protein (see AAW63123). It was isolated from a
CC   breast cancer cDNA library following an EST search for novel genes
CC   differentially expressed in breast cancer versus healthy breast tissue.
CC   The clone is deposited at ATCC 97175 and ATCC 97856. A gradient and stage
CC   -specific BCSG1 expression has been demonstrated from virtually no
CC   detectable expression in normal or benign breast to low level and partial
CC   expression in low grade in situ breast carcinoma and high expression in
CC   infiltrating malignant breast carcinomas. BCSG1 is useful as a breast
CC   cancer progression marker. Recombinant vectors and host cells useful for
CC   recombinant production of BCSG1 polypeptides (including epitope- bearing
CC   polypeptides) are provided. BCSG1 polynucleotides, polypeptides and
CC   antibodies can be used for the detection of breast cancer cells or breast
CC   cancer metastasis, and to develop methods for the clinical management and
CC   treatment of breast cancer
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.79e-60        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-017-715A-2 (1-127) x AAV42669 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 2
AAA39470
ID   AAA39470 standard; DNA; 550 BP.
XX
AC   AAA39470;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Human HBGBA67A DNA.
XX
KW   Human; ADA2; cytostatic; gene therapy; treatment; cancer;
KW   amyloid-like protein; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "HBGBA67"
XX
PN   US6054289-A.
XX
PD   25-APR-2000.
XX
PF   30-AUG-1996;   96US-00705771.
XX
PR   30-AUG-1995;   95US-0002993P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA;
XX
DR   WPI; 2000-338491/29.
DR   P-PSDB; AAY87779.
XX
PT   New polynucleotide encoding human AD2 is useful for treating cancer and
PT   for isolating cDNAs and genes having similar biological activity.
XX
PS   Disclosure; Col 27-28; 54pp; English.
XX
CC   This invention describes a novel polynucleotide (I) encoding human ADA2.
CC   The products of the invention have cytostatic activity and can be used
CC   for gene therapy. (I) is useful for treating cancer; as primers and
CC   probes for isolating full length cDNA and genes having similar biological
CC   activity. This sequence encodes a polypeptide derived from the human
CC   HBGBA67X clone which is an amyloid-like protein found in breast tissue
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.79e-60        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-09-017-715A-2 (1-127) x AAA39470 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311
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```
Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392
```

RESULT 3
ABL63343
ID ABL63343 standard; DNA; 550 BP.
XX
AC ABL63343;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:1680.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 1680; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.79e-60	Length:	550
Score:	610.00	Matches:	127
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-017-715A-2 (1-127) x ABL63343 (1-550)

```
Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392
```

```
RESULT 4
ABV73813
ID   ABV73813 standard; cDNA; 550 BP.
XX
AC   ABV73813;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human gamma-synuclein Glu110 variant gene.
XX
KW   Gamma-synuclein; human; single nucleotide polymorphism; SNP;
KW   schizophrenia; neuroleptic; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "Gamma-synuclein"
FT                   /transl_except= (pos:213. .215,aa:Glu)
FT   variation       replace(340,T)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200275317-A2.
XX
PD   26-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-EP002872.
XX
PR   15-MAR-2001; 2001US-0276306P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Roberts RC,  Van Oostrum J,  Voshol J,  Tamminga CA;
XX
DR   WPI; 2002-750574/81.
DR   P-PSDB; ABP54932.
XX
PT   Screening for compounds for treating or interfering with the onset of
PT   Schizophrenia Spectrum Disorders, by detecting interactions of candidate
PT   compounds with the gamma-synuclein polypeptide.
XX
PS   Disclosure; Fig 1; 32pp; English.
XX
CC   The present sequence is that of cDNA encoding the Glu-110 isoform of
CC   human gamma-synuclein. The invention relates to an isoform of gamma-
CC   synuclein that is caused by an A/T single nucleotide polymorphism (SNP)
CC   at position 329 of the gamma-synuclein coding sequence. This SNP causes a
CC   glutamic acid to valine change at amino acid position 110 of gamma-
CC   synuclein, and is associated with an increased susceptibility of
CC   individuals to schizophrenia spectrum disorders (SSDs). This is the first
CC   time that a genetic component of SSDs has been identified, and provides a
CC   potential target for diagnosis and treatment of schizophrenia. Gamma-
CC   synuclein polypeptides, especially those containing the E110V mutation,
CC   are used in a claimed method of screening for compounds useful for the
CC   treatment of SSDs, and gamma-synuclein expressing cells are used in a
CC   claimed method of screening for agonist or antagonist compounds. An
CC   oligonucleotide complementary to part of the gamma-synuclein coding
CC   sequence is used for the discrimination of an SNP at position 329 of the
CC   coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
CC   useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR
CC   amplification of a polynucleotide encoding gamma-synuclein and analysis
CC   of the occurrence of the SNP at position 329. A transgenic animal useful
CC   for the study of SSDs is also claimed
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.79e-60        Length:         550
Score:                  610.00          Matches:        127
%
```

```
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-017-715A-2 (1-127) x ABV73813 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 5
AAD63568
ID   AAD63568 standard; cDNA; 550 BP.
XX
AC   AAD63568;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human amyloid-like protein cDNA.
XX
KW   Human; genetic disease; muscular dystrophy; cystic fibrosis; cytostatic;
KW   scientific research; gene therapy; gene; amyloid-like protein; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "Human amyloid-like protein"
XX
PN   US6639052-B1.
XX
PD   28-OCT-2003.
XX
PF   14-OCT-1999;   99US-00417540.
XX
PR   30-AUG-1995;   95US-0002993P.
PR   30-AUG-1996;   96US-00705771.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA;
XX
DR   WPI; 2003-842790/78.
DR   P-PSDB; ABW02024.
XX
PT   New isolated protein and nucleic acid molecules, useful for diagnostic
PT   and therapeutic purposes, e.g. for treating genetic diseases such as
```

```
PT   muscular dystrophy or cystic fibrosis.
XX
PS   Example 5; Fig 1; 0pp; English.
XX
CC   The invention relates to isolated new isolated protein and nucleic acid
CC   molecules useful for diagnostic and therapeutic purposes. The invention
CC   is for treating genetic diseases such as muscular dystrophy or cystic
CC   fibrosis, and for in vitro purposes related to scientific research,
CC   synthesis of DNA and manufacture of DNA vectors. The invention is useful
CC   in gene therapy. The present sequence is human amyloid-like protein cDNA
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.79e-60        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-09-017-715A-2 (1-127) x AAD63568 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 6
ADG47636
ID   ADG47636 standard; cDNA; 550 BP.
XX
AC   ADG47636;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human amyloid like protein cDNA.
XX
KW   ss; gene; muscular dystrophy; cystic fibrosis; hypertension;
KW   angina pectoris; myocardial infarction; ulcer; asthma; allergy;
KW   psychosis; depression; migraine; vomiting; benign prostatic hypertrophy;
KW   osteoporosis; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag= a
FT                   /product= "Amyloid like protein"
XX
PN   US2003208043-A1.
XX
PD   06-NOV-2003.
XX
PF   04-JUN-2003; 2003US-00453478.
XX
PR   30-AUG-1995;   95US-0002993P.
PR   30-AUG-1996;   96US-00705771.
PR   14-OCT-1999;   99US-00417540.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA,  Gentz RL,  Ji H,  Ni J,  Hu J;
XX
DR   WPI; 2003-864796/80.
DR   P-PSDB; ADG47647.
XX
PT   New human polypeptides and polynucleotides, useful for diagnosing or
PT   treating genetic diseases such as muscular dystrophy or cystic fibrosis,
PT   hypertension, asthma, depression or osteoporosis.
XX
PS   Claim 18; SEQ ID NO 1; 56pp; English.
XX
CC   The invention relates to an isolated human polypeptide. The polypeptides,
CC   polynucleotides, agonists or antagonist are useful for diagnosing or
CC   treating genetic diseases such as muscular dystrophy or cystic fibrosis,
CC   hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
CC   allergies, psychoses, depression, migraine, vomiting, benign prostatic
CC   hypertrophy or osteoporosis. The polypeptides and polynucleotides are
CC   useful for in vitro purposes related to scientific research, synthesis of
CC   DNA and manufacture of DNA vector. The present sequence represents cDNA
CC   encoding human amyloid like protein.
XX
SQ   Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.79e-60        Length:         550
Score:                  610.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-09-017-715A-2 (1-127) x ADG47636 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392
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RESULT 7
ABV73915
ID   ABV73915 standard; cDNA; 550 BP.
XX
AC   ABV73915;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human gamma-synuclein Val110 variant gene.
XX
KW   Gamma-synuclein; human; single nucleotide polymorphism; SNP;
KW   schizophrenia; neuroleptic; mutant; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .395
FT                   /*tag=  a
FT                   /product= "Gamma-synuclein"
FT                   /transl_except= (pos:213. .215,aa:Glu)
FT   variation       replace(340,A)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200275317-A2.
XX
PD   26-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-EP002872.
XX
PR   15-MAR-2001; 2001US-0276306P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Roberts RC,  Van Oostrum J,  Voshol J,  Tamminga CA;
XX
DR   WPI; 2002-750574/81.
DR   P-PSDB; ABP54933.
XX
PT   Screening for compounds for treating or interfering with the onset of
PT   Schizophrenia Spectrum Disorders, by detecting interactions of candidate
PT   compounds with the gamma-synuclein polypeptide.
XX
PS   Disclosure; Page; 32pp; English.
XX
CC   The present sequence is that of cDNA encoding the Val-110 isoform of
CC   human gamma-synuclein. The invention relates to an isoform of gamma-
CC   synuclein that is caused by an A/T single nucleotide polymorphism (SNP)
CC   at position 329 of the gamma-synuclein coding sequence. This SNP causes a
CC   glutamic acid to valine change at amino acid position 110 of gamma-
CC   synuclein, and is associated with an increased susceptibility of
CC   individuals to schizophrenia spectrum disorders (SSDs). This is the first
CC   time that a genetic component of SSDs has been identified, and provides a
CC   potential target for diagnosis and treatment of schizophrenia. Gamma-
CC   synuclein polypeptides, especially those containing the E110V mutation,
CC   are used in a claimed method of screening for compounds useful for the
CC   treatment of SSDs, and gamma-synuclein expressing cells are used in a
CC   claimed method of screening for agonist or antagonist compounds. An
CC   oligonucleotide complementary to part of the gamma-synuclein coding
CC   sequence is used for the discrimination of an SNP at position 329 of the
CC   coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
CC   useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR
CC   amplification of a polynucleotide encoding gamma-synuclein and analysis
CC   of the occurrence of the SNP at position 329. A transgenic animal useful
CC   for the study of SSDs is also claimed. Note: The present sequence is not
CC   shown in the specification but is derived from the gamma-synuclein
CC   sequence given in Fig 1 (see ABV73813)
XX
SQ   Sequence 550 BP; 131 A; 145 C; 192 G; 82 T; 0 U; 0 Other;

Alignment Scores:
```

```
Pred. No.:              4.22e-59      Length:          550
Score:                  603.00        Matches:         126
Percent Similarity:     99.21%        Conservative:    0
Best Local Similarity:  99.21%        Mismatches:      1
Query Match:            98.85%        Indels:          0
DB:                     6             Gaps:            0

US-09-017-715A-2 (1-127) x ABV73915 (1-550)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392
```

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RESULT 8
AAI93778
ID   AAI93778 standard; cDNA; 783 BP.
XX
AC   AAI93778;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 13838.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US004927.
XX
PR   28-FEB-2000; 2000US-00515126.
PR   18-MAY-2000; 2000US-00577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   P-PSDB; AAO13847.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT   and treating e.g. leukemia, inflammation and immune disorders.
XX
```

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PS   Claim 1; SEQ ID NO 13838; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 783 BP; 187 A; 232 C; 237 G; 127 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.64e-59        Length:          783
Score:                    602.00          Matches:         125
Percent Similarity:       100.00%         Conservative:    2
Best Local Similarity:    98.43%          Mismatches:      0
Query Match:              98.69%          Indels:          0
DB:                       4               Gaps:            0

US-09-017-715A-2 (1-127) x AAI93778 (1-783)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        114 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 173

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 233

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 293

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        294 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 353

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 413

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 473

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        474 GAGGCCCAGAGTGGGGGAGAC 494

RESULT 9
AAF21784
ID   AAF21784 standard; DNA; 796 BP.
XX
AC   AAF21784;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 171.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055173-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005881.
XX
PR   12-MAR-1999;   99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   P-PSDB; AAB58881.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by these genes, useful in the prevention, treatment
PT   and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT   neurological diseases.
XX
PS   Claim 1; Page 608; 1299pp; English.
XX
CC   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC   neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC   antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC   protein sequences are used in the diagnosis of cancer, particularly
CC   breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC   and agonists may also be used in the diagnosis, prevention and treatment
CC   of immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC   cardiovascular disorders such as myocardial ischaemias; wound healing;
CC   neurological diseases such as cerebral anoxia and epilepsy; and
CC   infectious diseases
XX
SQ   Sequence 796 BP; 195 A; 233 C; 240 G; 126 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:                8.82e-59        Length:          796
Score:                    602.00          Matches:         125
Percent Similarity:       100.00%         Conservative:    2
Best Local Similarity:    98.43%          Mismatches:      0
Query Match:              98.69%          Indels:          0
DB:                       3               Gaps:            0

US-09-017-715A-2 (1-127) x AAF21784 (1-796)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        109 ATGGATGTYTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 168

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 228

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 288

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        289 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 348
```

```
Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 408

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 468

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        469 GAGGCCCAGAGTGGGGGAGAC 489

RESULT 10
ADM66887
ID   ADM66887 standard; DNA; 488 BP.
XX
AC   ADM66887;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human homologue of murine adipocyte specific gamma synuclein DNA Seq 20.
XX
KW   human; adipocyte specific; gene; ds; adipose tissue; anti-obesity;
KW   high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW   adipogenesis; hypertension; cardiovascular disease; anorectic;
KW   antidiabetic; hypotensive; gamma synuclein.
XX
OS   Homo sapiens.
XX
PN   WO2004011618-A2.
XX
PD   05-FEB-2004.
XX
PF   29-JUL-2003; 2003WO-US023684.
XX
PR   29-JUL-2002; 2002US-0398785P.
PR   12-JUN-2003; 2003US-0478206P.
XX
PA   (HMGE-) HMGENE INC.
XX
PI   Chada K,  Chouinard R,  Ashar H,  Sayed AMD;
XX
DR   WPI; 2004-143846/14.
DR   P-PSDB; ADM67167.
XX
PT   Identifying adipocyte specific genes, useful for treating obesity or
PT   diabetes, and for identifying drug targets, by differential gene
PT   expression analysis between adipose tissue or stromal vascular tissue of
PT   mice of different genotypes.
XX
PS   Claim 11; SEQ ID NO 20; 91pp; English.
XX
CC   This invention relates to a novel method for identifying genes that are
CC   over-expressed in adipose tissue and as such it provides targets for anti
CC   -obesity pharmaceutical compositions. Specifically, it refers to a high
CC   mobility group I-C protein (HMGI-C) that is associated with obesity and
CC   is epistatic to leptin, furthermore, it refers to the ob gene where an
CC   autosomal recessive trait is linked to obesity and diabetes. The present
CC   invention describes performing differential gene expression analysis
CC   between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC   of any two different mice selected from a group consisting of wild-type,
CC   HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC   this method novel nucleotides and the encoded proteins thereof were
CC   identified that are adipocyte specific, and as such can be used for
CC   preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC   hypertension and cardiovascular disease, as well as screening for
CC   compounds that can modulate or prevent adipogenesis and treat diabetes or
CC   obesity. These compositions exhibit anorectic, antidiabetic and
CC   hypotensive activities. This polynucleotide sequence is a human homologue
CC   of a murine adipocyte specific DNA sequence of the invention.
XX
SQ   Sequence 488 BP; 127 A; 119 C; 176 G; 66 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.92e-58      Length:          488
Score:                    595.00        Matches:         124
Percent Similarity:       99.21%        Conservative:    2
Best Local Similarity:    97.64%        Mismatches:      1
Query Match:              97.54%        Indels:          0
DB:                       12            Gaps:            0

US-09-017-715A-2 (1-127) x ADM66887 (1-488)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||:::|||||||||   |||||||||
Db         12 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGATGCGGTGGAA 71

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 131

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        192 GAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 371

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        372 GAGGCCCAGAGTGGGGGAGAC 392

RESULT 11
AAX29997
ID   AAX29997 standard; DNA; 720 BP.
XX
AC   AAX29997;
XX
DT   06-JUL-1999  (first entry)
XX
DE   Human persyn gene.
XX
KW   Human; synuclein; persyn; diagnosis; neurodegenerative disorder; cancer;
KW   breast; skin; intermediate filament damage; ss.
XX
OS   Homo sapiens.
XX
PN   EP908727-A1.
XX
PD   14-APR-1999.
XX
PF   21-SEP-1998;   98EP-00307628.
XX
PR   19-SEP-1997;   97GB-00019879.
XX
PA   (NEUR-) NEUROPA LTD.
PA   (UYSA-) UNIV ST ANDREWS.
XX
DR   WPI; 1999-217169/19.
DR   P-PSDB; AAY07271.
XX
PT   New synuclein protein (persyn) and gene, useful in assays for screening,
PT   diagnosing or monitoring cancer, neurodegenerative disorders or skin
PT   disorders.
XX
PS   Claim 29; Page 16-17; 39pp; English.
```

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XX
CC   This sequence represents the gene encoding a novel human synuclein family
CC   member designated persyn. The sequence is useful for screening,
CC   diagnosing or monitoring cancer (especially breast or skin cancer),
CC   neurodegenerative disorders or skin disorders and for identifying cells
CC   having intermediate filament damage
XX
SQ   Sequence 720 BP; 173 A; 209 C; 215 G; 123 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.82e-58        Length:         720
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     2               Gaps:           0

US-09-017-715A-2 (1-127) x AAX29997 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         49 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 12
ABS76519
ID   ABS76519 standard; cDNA; 720 BP.
XX
AC   ABS76519;
XX
DT   11-DEC-2002  (first entry)
XX
DE   cDNA encoding human ovarian cancer marker OV60.
XX
KW   Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW   central nervous system disorder; bacterial meningitis; viral meningitis;
KW   Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW   brain herniation; inflammation; encephalitis; testicular disorder;
KW   nontuberculous granulomatous orchitis; connective tissue disorder;
KW   heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW   histological type; carcinogenic; ovarian cancer marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200271928-A2.
XX
PD   19-SEP-2002.
XX
PF   14-MAR-2002; 2002WO-US007826.
XX
PR   14-MAR-2001; 2001US-0276025P.
PR   14-MAR-2001; 2001US-0276026P.
PR   10-AUG-2001; 2001US-0311732P.
PR   19-SEP-2001; 2001US-0323580P.
PR   26-SEP-2001; 2001US-0324967P.
PR   26-SEP-2001; 2001US-0325102P.
PR   26-SEP-2001; 2001US-0325149P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Monahan JE,  Gannavarapu M,  Hoersch S,  Kamatkar S,  Kovatis SG;
PI   Meyers RE,  Morrisey MP,  Olandt PJ,  Sen A,  Vieby PO,  Mills GB;
PI   Bast RC,  Lu K,  Schmandt RE,  Zhao X,  Glatt K;
XX
DR   WPI; 2002-723277/78.
DR   P-PSDB; ABG96420.
XX
PT   Assessing whether a patient is afflicted with ovarian cancer, useful in
PT   assessing the stage or progression of the disease, comprises comparing
PT   the expression level of a cancer marker in a sample from a patient and
PT   from a non cancer patient.
XX
PS   Disclosure; Page 411; 481pp; English.
XX
CC   The present invention relates to a new method for assessing whether a
CC   patient is afflicted with ovarian cancer. The method involves comparing
CC   the expression level of a marker in a patient sample and the normal level
CC   of expression of the marker in a control non-ovarian cancer sample, where
CC   the marker is selected from 363 cancer markers described in the
CC   specification. The method of the invention is useful in diagnosing or
CC   characterising cancer, in detecting the presence of cancer as early as
CC   possible, and the recurrence of ovarian cancer. The method may also be of
CC   particular use with patients having an enhanced risk of developing
CC   ovarian cancer (e.g. patients having a familial history of ovarian
CC   cancer). The cancer markers may be used in the management and treatment
CC   of e.g. brain and central nervous system disorders (e.g. bacterial and
CC   viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC   disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
CC   inflammations (e.g. bacterial or viral meningitis or encephalitis),
CC   testicular disorders (e.g. nontuberculous granulomatous orchitis),
CC   connective tissue disorders, or heart disorders (e.g. ischaemic heart
CC   disease or atherosclerosis). The compositions and methods may also be
CC   used in assessing the histological type of neoplasm associated with
CC   ovarian cancer, monitoring the progression of ovarian cancer, determining
CC   whether ovarian cancer has metastasized or is likely to metastasize,
CC   selecting a composition for inhibiting ovarian cancer, assessing the
CC   ovarian carcinogenic potential of a compound, or inhibiting ovarian
CC   cancer or at risk of developing ovarian cancer. The present nucleic acid
CC   sequence encodes one of the ovarian cancer markers described in the
CC   invention
XX
SQ   Sequence 720 BP; 173 A; 209 C; 215 G; 123 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.82e-58        Length:         720
Score:                  595.00          Matches:        124
Percent Similarity:     99.21%          Conservative:   2
Best Local Similarity:  97.64%          Mismatches:     1
Query Match:            97.54%          Indels:         0
DB:                     6               Gaps:           0

US-09-017-715A-2 (1-127) x ABS76519 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         49 ATGGATGTCTTCAAGAAGGGCTTCTCCATCGCCAAGGAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 13
ADE43864
ID   ADE43864 standard; cDNA; 720 BP.
XX
AC   ADE43864;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human SNCG cDNA, SEQ ID 469.
XX
KW   Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW   Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW   Chromosome 10; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003054143-A2.
XX
PD   03-JUL-2003.
XX
PF   25-OCT-2002; 2002WO-US034679.
XX
PR   25-OCT-2001; 2001US-0339525P.
PR   08-NOV-2001; 2001US-0336929P.
PR   08-NOV-2001; 2001US-0338010P.
PR   09-NOV-2001; 2001US-0338363P.
PR   04-DEC-2001; 2001US-0337052P.
PR   28-MAR-2002; 2002US-0368919P.
XX
PA   (NEUR-) NEUROGENETICS INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI   Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR   WPI; 2003-559131/52.
XX
PT   Determining a predisposition for or the occurrence of neurodegenerative
PT   disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT   the presence or absence of an allelic variant of one or more polymorphic
PT   regions.
XX
PS   Claim 84; Page 740; 848pp; English.
XX
CC   The present invention relates to a method (M1) for determining a
CC   predisposition for or the occurrence of neurodegenerative disease in a
CC   subject. The method comprises detecting in a target nucleic acid obtained
CC   from the subject the presence or absence of an allelic variant of one or
CC   more polymorphic regions of one or more genes selected from uPA
CC   (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC   degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
CC   lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC   presence of at least one of the allelic variant of one or more
CC   polymorphic regions is indicative of a predisposition for or the
CC   occurrence of neurodegenerative disease. The genes are all located on
CC   chromosome 10. M1 is useful for determining a predisposition for or the
CC   occurrence of, and for treating neurodegenerative disease, particularly
CC   Alzheimer's disease.
XX
SQ   Sequence 720 BP; 172 A; 205 C; 212 G; 120 T; 0 U; 11 Other;

Alignment Scores:
Pred. No.:              1.05e-57      Length:          720
Score:                  592.00        Matches:         124
Percent Similarity:     97.64%        Conservative:    0
Best Local Similarity:  97.64%        Mismatches:      3
Query Match:            97.05%        Indels:          0
DB:                     10            Gaps:            0

US-09-017-715A-2 (1-127) x ADE43864 (1-720)

Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db         49 ATGGATGTNTTCAAGAAGGGCTTCTCCATCGCCAAGNAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCNGTGAGCNAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              |||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGNGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429

RESULT 14
ADH54342
ID   ADH54342 standard; cDNA; 720 BP.
XX
AC   ADH54342;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human SNCG gene cDNA sequence SeqID469.
XX
KW   human; neurodegenerative disease; urokinase plasminogen activator; uPA;
KW   gamma-synuclein; SNCG; insulin degrading enzyme; IDE;
KW   kinesin-like protein 1; KNSL1; lysosomal acid lipase; LIPA;
KW   tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; ss.
XX
OS   Homo sapiens.
XX
PN   US2003224380-A1.
XX
PD   04-DEC-2003.
XX
PF   25-OCT-2002; 2002US-00282174.
XX
PR   25-OCT-2001; 2001US-0339525P.
PR   25-OCT-2001; 2001US-0348065P.
PR   02-NOV-2001; 2001US-0336983P.
PR   08-NOV-2001; 2001US-0336929P.
PR   08-NOV-2001; 2001US-0338010P.
PR   09-NOV-2001; 2001US-0338363P.
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PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Becker KD, Velicelebi G, Ellliott KJ, Wang X, Tanzi RE;
PI Bertram L, Saunders AJ, Mullin KM, Sampson AJ;
XX
DR WPI; 2004-060538/06.
XX
PT Determining a predisposition for or the occurrence of neurodegenerative
PT disease, particularly Alzheimer's disease, comprises determining the
PT presence of a polymorphism in the uPA, SNCG, IDE, KNSL1, LIPA or TNFRSF6
PT gene.
XX
PS Claim 84; SEQ ID NO 469; 205pp; English.
XX
CC This invention relates to a novel method of determining a predisposition
CC for or the occurrence of neurodegenerative disease comprising detecting
CC in a target nucleic acid obtained from the subject the presence of an
CC allelic variant of polymorphic regions of human genes selected from
CC urokinase plasminogen activator (uPA), gamma-synuclein (SNCG), insulin
CC degrading enzyme (IDE), kinesin-like protein 1 (KNSL1), lysosomal acid
CC lipase (LIPA) and tumour necrosis factor receptor SF6 (TNFRSF6). The
CC method is useful in determining the presence or predisposition to a
CC neurodegenerative disease, particularly Alzheimer's disease. The present
CC sequence is the cDNA sequence of the human SNCG gene which is related to
CC the invention.
XX
SQ Sequence 720 BP; 172 A; 205 C; 212 G; 120 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.:	1.05e-57	Length:	720
Score:	592.00	Matches:	124
Percent Similarity:	97.64%	Conservative:	0
Best Local Similarity:	97.64%	Mismatches:	3
Query Match:	97.05%	Indels:	0
DB:	12	Gaps:	0

US-09-017-715A-2 (1-127) x ADH54342 (1-720)

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Qy          1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db         49 ATGGATGTNTTCAAGAAGGGCTTCTCCATCGCCAAGNAGGGCGTGGTGGGTGCGGTGGAA 108

Qy         21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 AAGACCAAGCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGTG 168

Qy         41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 228

Qy         61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        229 GAGCAGGCCAACGCNGTGAGCNAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 288

Qy         81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 348

Qy        101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        349 AGGCCATCTGCCCCCCAACAGGAGGGTGNGGCATCCAAAGAGAAAGAGGAAGTGGCAGAG 408

Qy        121 GluAlaGlnSerGlyGlyAsp 127
              |||||||||||||||||||
Db        409 GAGGCCCAGAGTGGGGGAGAC 429
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RESULT 15
ACH15493
ID ACH15493 standard; cDNA; 479 BP.
XX
AC ACH15493;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult brain cDNA #2705.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 2705; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 479 BP; 120 A; 118 C; 178 G; 56 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	8.23e-52	Length:	479
Score:	538.00	Matches:	112
Percent Similarity:	99.14%	Conservative:	3
Best Local Similarity:	96.55%	Mismatches:	1
Query Match:	88.20%	Indels:	0
DB:	9	Gaps:	0

US-09-017-715A-2 (1-127) x ACH15493 (1-479)

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Qy         12 LysLysGlyValValGlyAlaValGluLysThrLysGlnGlyValThrGluAlaAlaGlu 31
              ::::::||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db         47 CAGGAGGGCGTGGNGGGTGCGGTGGAAAAGACCAAGCAGGGGGTGACGGAAGCAGCTGAG 106

Qy         32 LysThrLysGluGlyValMetTyrValGlyAlaLysThrLysGluAsnValValGlnSer 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 AAGACCAAGGAGGGGGTCATGTATGTGGGAGCCAAGACCAAGGAGAATGTTGTACAGAGC 166
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Qy          52 ValThrSerValAlaGluLysThrLysGluGlnAlaAsnAlaValSerLysAlaValVal 71
               ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db         167 GTGACCTCAGTGGCCGAGAAGACCAAGGAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTG 226

Qy          72 SerSerValAsnThrValAlaThrLysThrValGluGluAlaGluAsnIleAlaValThr 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         227 AGCAGCGTCAACACTGTGGCCACCAAGACCGTGGAGGAGGCGGAGAACATCGCGGTCACC 286

Qy          92 SerGlyValValArgLysGluAspLeuArgProSerAlaProGlnGlnGluGlyGluAla 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         287 TCCGGGGTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAGGAGGGTGAGGCA 346

Qy         112 SerLysGluLysGluGluValAlaGluGluAlaGlnSerGlyGlyAsp 127
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         347 TCCAAAGAGAAAGAGGAAGTGGCAGAGGAGGCCCAGAGTGGGGGAGAC 394
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Search completed: May 4, 2005, 09:26:16
Job time : 934.208 secs